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OM protein - protein search, using sw model

Run on: February 19, 2004, 19:49:48 ; Search time 39 Seconds

(without alignments)  
4321.865 Million cell updates/sec

Title: US-09-163-648-2

Perfect score: 4291

Sequence: 1 MSSSSWLLSLVAVTAQAQT.....ISKGNNGPGFQNTDDVQTSF 805

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	4291	100.0	805	10	US-09-978-385-2
2	4291	100.0	805	12	US-10-158-825-142
3	4291	100.0	805	15	US-10-158-847-142
4	4291	100.0	805	15	US-10-005-956-570
5	4291	100.0	805	15	US-10-005-956-843
6	4287	99.9	805	14	US-10-114-893-86
7	3775	88.0	711	10	US-09-969-384-13
8	3775	88.0	711	12	US-10-158-825-138
9	3775	88.0	711	15	US-10-158-847-138
10	3643	84.9	681	10	US-09-969-384-25
11	3643	84.9	681	12	US-10-158-825-140
12	3643	84.9	681	15	US-10-158-847-140
13	3579	83.4	805	10	US-09-978-385-6
14	3561	83.0	805	10	US-09-978-385-9
15	2979	69.4	555	12	US-10-137-870-72

16	2979	69.4	555	12	US-10-140-018-72	Sequence 72, Appl
17	2979	69.4	555	12	US-10-140-021-72	Sequence 72, Appl
18	2979	69.4	555	12	US-10-140-274-72	Sequence 72, Appl
19	2979	69.4	555	12	US-10-140-471-72	Sequence 72, Appl
20	2979	69.4	555	12	US-10-140-807-72	Sequence 72, Appl
21	2979	69.4	555	12	US-10-140-922-72	Sequence 72, Appl
22	2979	69.4	555	12	US-10-140-924-72	Sequence 72, Appl
23	2979	69.4	555	12	US-10-140-926-72	Sequence 72, Appl
24	2979	69.4	555	12	US-10-141-698-72	Sequence 72, Appl
25	2979	69.4	555	12	US-10-141-702-72	Sequence 72, Appl
26	2979	69.4	555	12	US-10-141-704-72	Sequence 72, Appl
27	2979	69.4	555	12	US-10-142-421-72	Sequence 72, Appl
28	2979	69.4	555	12	US-10-142-432-72	Sequence 72, Appl
29	2979	69.4	555	12	US-10-142-767-72	Sequence 72, Appl
30	2979	69.4	555	12	US-10-143-033-72	Sequence 72, Appl
31	2979	69.4	555	12	US-10-144-994-72	Sequence 72, Appl
32	2979	69.4	555	12	US-10-145-628-72	Sequence 72, Appl
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34	2979	69.4	555	12	US-10-145-633-72	Sequence 72, Appl
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36	2979	69.4	555	12	US-10-145-748-72	Sequence 72, Appl
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38	2979	69.4	555	12	US-10-145-826-72	Sequence 72, Appl
39	2979	69.4	555	12	US-10-145-870-72	Sequence 72, Appl
40	2979	69.4	555	12	US-10-145-876-72	Sequence 72, Appl
41	2979	69.4	555	12	US-10-145-959-72	Sequence 72, Appl
42	2979	69.4	555	12	US-10-146-724-72	Sequence 72, Appl
43	2979	69.4	555	12	US-10-146-725-72	Sequence 72, Appl
44	2979	69.4	555	12	US-10-146-795-72	Sequence 72, Appl
45	2979	69.4	555	12	US-10-147-495-72	Sequence 72, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-978-385-2 ; Sequence 2, Application US/09978385  
; Patent No. US2002017721A1  
; GENERAL INFORMATION:  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Petrie, Charles  
; APPLICANT: Shoemaker, Kimberly B.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME  
; FILE REFERENCE: 99-24C1  
; CURRENT APPLICATION NUMBER: 60/133,952  
; PRIOR FILING DATE: 2001-10-16  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR FILING DATE: 60/151,181  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR FILING DATE: 09/563,516  
; PRIOR FILING DATE: 2000-05-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 805  
; TYPE: PRI  
; ORGANISM: Homo sapiens  
US-09-978-385-2

Query Match 100.0%; Score 4291; DB 10; Length 805;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSSSSWLLSLVAVTAQAQTIEEQAKTELDKFNHAEEDLFYQSSLASWYNTNITEENVQ	60
Db	1	MSSSSWLLSLVAVTAQAQTIEEQAKTELDKFNHAEEDLFYQSSLASWYNTNITEENVQ	60
Qy	61	MNNAGDKNSAFLKEQSTLAQMYFLOEIQNLTVKQLQALQONGSSVLSEDKSKRLNTIL	120
Db	61	MNNAGDKNSAFLKEQSTLAQMYFLOEIQNLTVKQLQALQONGSSVLSEDKSKRLNTIL	120

QY 121 NTMTIYTGKVCNPNPQECCLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180  
DB 121 NTMTIYTGKVCNPNPQECCLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180  
QY 181 EYVVLKNEMARANHYEDYDGYWGDYEVNGVDYDYSRGOLTEDEHTEETEEIKPLYEHL 240  
DB 181 EYVVLKNEMARANHYEDYDGYWGDYEVNGVDYDYSRGOLTEDEHTEETEEIKPLYEHL 240  
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DB 241 HAYVRALKNMAYPSYISPIGCLPAHLLGDMWGRFTWNLVSLTVFPFGKPNIDVTDAMVDQ 300  
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DB 301 AWDQRIIFKEAEKFFVSVGLPNNTOGFWENSMITDPGNVQKAVCHPTAWDLGKGFRLM 360  
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DB 361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
QY 421 IGLSPDFQEDNETEINFLLKQALTIIVGTLPTTYMLEKRWMMVFKGEIPKQOMKKWEM 480  
DB 421 IGLSPDFQEDNETEINFLLKQALTIIVGTLPTTYMLEKRWMMVFKGEIPKQOMKKWEM 480  
QY 481 KREIVGVVPEPHDETYCDPASLFHVSNDYSFIRYRTLYQFQOEALCOAAKHEGPHL 540  
DB 481 KREIVGVVPEPHDETYCDPASLFHVSNDYSFIRYRTLYQFQOEALCOAAKHEGPHL 540  
QY 541 KCDISNSTEAGOKLFNMLRGKSEBWTALENVVGAKNMVRPLNLYFEPLFTWLKDQNK 600  
DB 541 KCDISNSTEAGOKLFNMLRGKSEBWTALENVVGAKNMVRPLNLYFEPLFTWLKDQNK 600  
QY 601 NSFVGNSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMROYFLVKVN 660  
DB 601 NSFVGNSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMROYFLVKVN 660  
QY 661 QMILFGEEDVRVANLKPRIISFNFFVTAPKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720  
DB 661 QMILFGEEDVRVANLKPRIISFNFFVTAPKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720  
QY 721 SLEFLGIQTLGPPNPPVSIWLVFGVVMGVIVGVILIFTGIRDRKKKCKKARSGENP 780  
DB 721 SLEFLGIQTLGPPNPPVSIWLVFGVVMGVIVGVILIFTGIRDRKKKCKKARSGENP 780  
QY 781 YASIDISKGENNPGFQNTDDVQTSF 805  
DB 781 YASIDISKGENNPGFQNTDDVQTSF 805

RESULT 2  
US-10-158-825-142  
; Sequence 142, Application US/10158825  
; Publication No. US20030138894A1  
; GENERAL INFORMATION:  
; APPLICANT: Tom Parry et al.  
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity  
; FILE REFERENCE: PF555  
; CURRENT APPLICATION NUMBER: US/10/158,825  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 60/294,976  
; PRIOR FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 158  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 142  
; LENGTH: 805  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-158-825-142

Query Match 100.0%; Score 4291; DB 12; Length 805;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSSSWLLLSLVAVTAQSTTBEQAKTFELDKFNEAEDLFYQSSLASWNYNTNITEENVQ 60  
QY 61 NNNAGDKWSAFLKEQSTLAQMYPLQEIQNTLVKQLQALQOQSSVLSSEKSKRLNTIL 120  
DB 61 NNNAGDKWSAFLKEQSTLAQMYPLQEIQNTLVKQLQALQOQSSVLSSEKSKRLNTIL 120  
QY 121 NTMTIYTGKVCNPNPQECCLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180  
DB 121 NTMTIYTGKVCNPNPQECCLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180  
QY 181 EYVVLKNEMARANHYEDYDGYWGDYEVNGVDYDYSRGOLTEDEHTEETEEIKPLYEHL 240  
DB 181 EYVVLKNEMARANHYEDYDGYWGDYEVNGVDYDYSRGOLTEDEHTEETEEIKPLYEHL 240  
QY 241 HAYVRALKNMAYPSYISPIGCLPAHLLGDMWGRFTWNLVSLTVFPFGKPNIDVTDAMVDQ 300  
DB 241 HAYVRALKNMAYPSYISPIGCLPAHLLGDMWGRFTWNLVSLTVFPFGKPNIDVTDAMVDQ 300  
QY 301 AWDQRIIFKEAEKFFVSVGLPNNTOGFWENSMITDPGNVQKAVCHPTAWDLGKGFRLM 360  
DB 301 AWDQRIIFKEAEKFFVSVGLPNNTOGFWENSMITDPGNVQKAVCHPTAWDLGKGFRLM 360  
QY 361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
DB 361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
QY 421 IGLSPDFQEDNETEINFLLKQALTIIVGTLPTTYMLEKRWMMVFKGEIPKQOMKKWEM 480  
DB 421 IGLSPDFQEDNETEINFLLKQALTIIVGTLPTTYMLEKRWMMVFKGEIPKQOMKKWEM 480  
QY 481 KREIVGVVPEPHDETYCDPASLFHVSNDYSFIRYRTLYQFQOEALCOAAKHEGPHL 540  
DB 481 KREIVGVVPEPHDETYCDPASLFHVSNDYSFIRYRTLYQFQOEALCOAAKHEGPHL 540  
QY 541 KCDISNSTEAGOKLFNMLRGKSEBWTALENVVGAKNMVRPLNLYFEPLFTWLKDQNK 600  
DB 541 KCDISNSTEAGOKLFNMLRGKSEBWTALENVVGAKNMVRPLNLYFEPLFTWLKDQNK 600  
QY 601 NSFVGNSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMROYFLVKVN 660  
DB 601 NSFVGNSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMROYFLVKVN 660  
QY 661 QMILFGEEDVRVANLKPRIISFNFFVTAPKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720  
DB 661 QMILFGEEDVRVANLKPRIISFNFFVTAPKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720  
QY 721 SLEFLGIQTLGPPNPPVSIWLVFGVVMGVIVGVILIFTGIRDRKKKCKKARSGENP 780  
DB 721 SLEFLGIQTLGPPNPPVSIWLVFGVVMGVIVGVILIFTGIRDRKKKCKKARSGENP 780  
QY 781 YASIDISKGENNPGFQNTDDVQTSF 805  
DB 781 YASIDISKGENNPGFQNTDDVQTSF 805

RESULT 3  
US-10-158-847-142  
; Sequence 142, Application US/10158847  
; Publication No. US20030091557A1  
; GENERAL INFORMATION:  
; APPLICANT: Tom Parry et al.  
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity  
; FILE REFERENCE: PF557  
; CURRENT APPLICATION NUMBER: US/10/158,847  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 60/295,004  
; PRIOR FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 158  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 142

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; LENGTH: 805
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-142

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSSSSWLLLSLVAVTAQAOSTIEQAKTFLDKFNHAEADLFYQSSLASWNTNTITEENVQ 60

Qy 61 NNNAGDKWSAFLEKEQSTLAQMYPLQEIQNLTVKLQALQONGSSVLSDESKRLNTIL 120
Db 61 NNNAGDKWSAFLEKEQSTLAQMYPLQEIQNLTVKLQALQONGSSVLSDESKRLNTIL 120

Qy 121 NTMTSTIYSTGKVCNPNPOECCLLEPGLNEIMANSLDYNERLWAWESWRSVGVKQLRPLY 180
Db 121 NTMTSTIYSTGKVCNPNPOECCLLEPGLNEIMANSLDYNERLWAWESWRSVGVKQLRPLY 180

Qy 181 EYVVLKNEMARANHVEDYDGYWRGDYEVNGVDGYDSRGQIIEDEVHTFEEIKPLYEHL 240
Db 181 EYVVLKNEMARANHVEDYDGYWRGDYEVNGVDGYDSRGQIIEDEVHTFEEIKPLYEHL 240

Qy 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMGWFNTLYSLTVPGQKPNIDVTAMDQ 300
Db 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMGWFNTLYSLTVPGQKPNIDVTAMDQ 300

Qy 301 AWAQRIKFEAEKFFVSVGLPNTQGFWENSLTDPGNVQKAVCHPTAWDLGKGFRLM 360
Db 301 AWAQRIKFEAEKFFVSVGLPNTQGFWENSLTDPGNVQKAVCHPTAWDLGKGFRLM 360

Qy 361 CTKVMTDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
Db 361 CTKVMTDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420

Qy 421 IGLSPDFQEDNETEINFLLKQALITVGLTPFTYMLEKRWVFKGEIPKQOMKKWEM 480
Db 421 IGLSPDFQEDNETEINFLLKQALITVGLTPFTYMLEKRWVFKGEIPKQOMKKWEM 480

Qy 481 KREIVGVVEVPDHDTEYCDPASLFHVSNDYSFIRYVTRTLTQFQOEALCOAAKHEGPLH 540
Db 481 KREIVGVVEVPDHDTEYCDPASLFHVSNDYSFIRYVTRTLTQFQOEALCOAAKHEGPLH 540

Qy 541 KCDISNSTEAGOKLFNMLRLGKSEPTLALENVGAKMNVRLPILNYPEPLFTWLKDQNK 600
Db 541 KCDISNSTEAGOKLFNMLRLGKSEPTLALENVGAKMNVRLPILNYPEPLFTWLKDQNK 600

Qy 601 NSFVGMSTDWSPYADQSIKVRISLKSALGDKAYEWNNDNMYLFRSSVAYAMRQYFLKVK 660
Db 601 NSFVGMSTDWSPYADQSIKVRISLKSALGDKAYEWNNDNMYLFRSSVAYAMRQYFLKVK 660

Qy 661 QMILFGEEDVRVANLKPRISFNFFVAPKNVSDIIPRTEVEKAIKRSRINDAFRLND 720
Db 661 QMILFGEEDVRVANLKPRISFNFFVAPKNVSDIIPRTEVEKAIKRSRINDAFRLND 720

Qy 721 SLEFLGIQPTLGGPPNPQPVSIWLVGVGMVGVVGVVGVVGVVGVVGVVGVVGVVGVV 780
Db 721 SLEFLGIQPTLGGPPNPQPVSIWLVGVGMVGVVGVVGVVGVVGVVGVVGVVGVVGVV 780

Qy 781 YASIDISKGNPNPGONTDDVQTSF 805
Db 781 YASIDISKGNPNPGONTDDVQTSF 805

RESULT 4
US-10-005-956-570
; Sequence 570, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
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QY 781 YASIDISGENNPGFQNTDDVQTSF 805  
Db 781 YASIDISGENNPGFQNTDDVQTSF 805

RESULT 5  
US-10-005-956-843  
; Sequence 843, Application US/10005956  
; Publication No. US20030113726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005,956  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 843  
; LENGTH: 805  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-005-956-843

Query Match 100.0%; Score 4291; DB 15; Length 805;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSSSSWLLLSLVAVTAQAQSTIEEQAKTFDKNHEADLFYQSSLASWYNNTNITEENVQ 60

QY 61 NNNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSSEKSKRLNTIL 120  
Db 61 NNNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSSEKSKRLNTIL 120

QY 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVKGQRLPLY 180  
Db 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVKGQRLPLY 180

QY 181 EYVVLKNEARANHVEDYDGRGVDYVNGVDYDGRGQIEDVEHTEFEIKPLYEHL 240  
Db 181 EYVVLKNEARANHVEDYDGRGVDYVNGVDYDGRGQIEDVEHTEFEIKPLYEHL 240

QY 241 HAYVRKLMNAYPSYISPIGCLPAHLLGDMWGRFNTNLSLTVPFGQKPNIDVTAMVDQ 300  
Db 241 HAYVRKLMNAYPSYISPIGCLPAHLLGDMWGRFNTNLSLTVPFGQKPNIDVTAMVDQ 300

QY 301 AWAQRIEKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDLGKGFRIIM 360  
Db 301 AWAQRIEKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDLGKGFRIIM 360

QY 361 CTKVWDDFLTAHEMGHIQYDWAYAAQPFLLRNGANEGFHAAGVIMSLSAATPKHLS 420  
Db 361 CTKVWDDFLTAHEMGHIQYDWAYAAQPFLLRNGANEGFHAAGVIMSLSAATPKHLS 420

QY 421 IGLSPDFQDNTEINFLLKQALTIVGTLPTFTMLKRWVWVFKGEI PKDQMKKQWEM 480  
Db 421 IGLSPDFQDNTEINFLLKQALTIVGTLPTFTMLKRWVWVFKGEI PKDQMKKQWEM 480

QY 481 KREIVGVVEVPVPHDETCDPASLFHVSNDYSFIRYVTRTLTQFQFQALCOAAKHEGPHL 540  
Db 481 KREIVGVVEVPVPHDETCDPASLFHVSNDYSFIRYVTRTLTQFQFQALCOAAKHEGPHL 540

QY 541 KDISNSTEAGOKLFNMLRGLKSEPTWLTALENVGAKMNVRLNLYFPLFTWLKDQNK 600  
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QY 601 NSFVGWSTDSWSPYADQSIKVRISLSKALGDKAYEWNDEMILFRSSVAYAMRQVFLKVK 660  
Db 601 NSFVGWSTDSWSPYADQSIKVRISLSKALGDKAYEWNDEMILFRSSVAYAMRQVFLKVK 660

QY 661 QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720  
Db 661 QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720

QY 721 SLEFLGIQPTLGPNNQPPVSIWLVGVVGMVIVVIGVILIFTGIRDRKKKKKARSGENP 780  
Db 721 SLEFLGIQPTLGPNNQPPVSIWLVGVVGMVIVVIGVILIFTGIRDRKKKKKARSGENP 780

QY 781 YASIDISGENNPGFQNTDDVQTSF 805  
Db 781 YASIDISGENNPGFQNTDDVQTSF 805

RESULT 6  
US-10-114-893-86  
; Sequence 86, Application US/10114893  
; Publication No. US20020193567A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: LaVallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Bowman, Michael R.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Carlin-Duckett, McKeough  
; APPLICANT: Kelleher, Kerry S.  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: GI 6000-10A  
; CURRENT APPLICATION NUMBER: US/10/114,893  
; CURRENT FILING DATE: 2002-04-02  
; EARLIER APPLICATION NUMBER: 09/413,232  
; EARLIER FILING DATE: 1999-10-06  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 805  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-114-893-86

Query Match 99.9%; Score 4287; DB 14; Length 805;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 804; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAQAQSTIEEQAKTFDKNHEADLFYQSSLASWYNNTNITEENVQ 60  
Db 1 MSSSSWLLLSLVAVTAQAQSTIEEQAKTFDKNHEADLFYQSSLASWYNNTNITEENVQ 60

QY 61 NNNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSSEKSKRLNTIL 120  
Db 61 NNNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSSEKSKRLNTIL 120

QY 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVKGQRLPLY 180  
Db 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVKGQRLPLY 180

QY 181 EYVVLKNEARANHVEDYDGRGVDYVNGVDYDGRGQIEDVEHTEFEIKPLYEHL 240  
Db 181 EYVVLKNEARANHVEDYDGRGVDYVNGVDYDGRGQIEDVEHTEFEIKPLYEHL 240

QY 241 HAYVRKLMNAYPSYISPIGCLPAHLLGDMWGRFNTNLSLTVPFGQKPNIDVTAMVDQ 300  
Db 241 HAYVRKLMNAYPSYISPIGCLPAHLLGDMWGRFNTNLSLTVPFGQKPNIDVTAMVDQ 300

QY 301 AWAQRIEKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDLGKGFRIIM 360

301 AWAQRIKAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHTAWDLGKGFRIILM 360  
361 CTKVTDMDFFTAHEMGGHIQYDMAYAAQPFLLRNGANEGHEAVGEIMSLSAATPKHLKS 420  
361 CTKVTDMDFFTAHEMGGHIQYDMAYAAQPFLLRNGANEGHEAVGEIMSLSAATPKHLKS 420  
421 IGLSPDFQEDNETEINFLKQALTIIVGTLPTFMYLKKRWVFKGEIPKQDQWKKWEM 480  
421 IGLSPDFQEDNETEINFLKQALTIIVGTLPTFMYLKKRWVFKGEIPKQDQWKKWEM 480  
481 KREIVGVVPEVPHDDETCDPASLPHVSNDSYFIRYTRTYLQFOEALCOAAKHEGPHLH 540  
481 KREIVGVVPEVPHDDETCDPASLPHVSNDSYFIRYTRTYLQFOEALCOAAKHEGPHLH 540  
541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLNLYFELFTWLDQNK 600  
541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLNLYFELFTWLDQNK 600  
601 NSFVGMSTDSPPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVN 660  
601 NSFVGMSTDSPPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVN 660  
661 QMILFGEDVRVANLKRISNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDN 720  
661 QMILFGEDVRVANLKRISNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDN 720  
721 SLEFLGIQPTLGPNNQPPVSIWLVFGVMGVIIVGVILIFTGIRDKKKARSGENP 780  
721 SLEFLGIQPTLGPNNQPPVSIWLVFGVMGVIIVGVILIFTGIRDKKKARSGENP 780  
781 YASIDISKGENNPGFQNTDDVQTSF 805  
781 YASIDISKGENNPGFQNTDDVQTSF 805

RESULT 7  
US-09-969-384-13  
; Sequence 13, Application US/09969384  
; Publication No. US20020192749A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore, et al.  
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies  
; CURRENT APPLICATION NUMBER: US/09/969,384  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: PCT/US01/10542  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: 60/236,384  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/194,118  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (219)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (240)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (499)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-969-384-13

Query Match 88.0%; Score 3775; DB 10; Length 711;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 704; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

62 MNAAGDKWSAFLKQSTLAQMYPLQEIQNLTKVLQALQONGSSVLSEDKSKRLNTILN 121  
1 MNAAGDKWSAFLKQSTLAQMYPLQEIQNLTKVLQALQONGSSVLSEDKSKRLNTILN 60  
122 TMTSTIYSTGKVCNPNPOBCLLLEPGLNEINMANSLDYNERLWAWESWRSEVKGQLRPLYE 181  
61 TMTSTIYSTGKVCNPNPOBCLLLEPGLNEINMANSLDYNERLWAWESWRSEVKGQLRPLYE 120  
182 EVVVLKNEAMARAHYEDYDGYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEIKPLYEHLH 241  
121 EVVVLKNEAMARAHYEDYDGYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEIKPLYEHLH 180  
242 AYVRAKLANVAPSYISPIGCLPAHLGDMGRFNTNLSYLVPGQKPNIDVTAMWDOA 301  
181 AYVRAKLANVAPSYISPIGCLPAHLGDMGRFNTNLSYLVPGQKPNIDVTAMWDOX 240  
302 WDAQRIKAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHTAWDLGKGFRIILMC 361  
241 WDAQRIKAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHTAWDLGKGFRIILMC 300  
362 TKVTMDDELTAHEMGGHIQYDMAYAAQPFLLRNGANEGHEAVGEIMSLSAATPKHLKSI 421  
301 TKVTMDDELTAHEMGGHIQYDMAYAAQPFLLRNGANEGHEAVGEIMSLSAATPKHLKSI 360  
422 GLLSPDFQEDNETEINFLKQALTIIVGTLPTFMYLKKRWVFKGEIPKQDQWKKWEMK 481  
361 GLLSPDFQEDNETEINFLKQALTIIVGTLPTFMYLKKRWVFKGEIPKQDQWKKWEMK 420  
482 REIVGVVPEVPHDDETCDPASLPHVSNDSYFIRYTRTYLQFOEALCOAAKHEGPHLH 541  
421 REIVGVVPEVPHDDETCDPASLPHVSNDSYFIRYTRTYLQFOEALCOAAKHEGPHLH 480  
542 CDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLNLYFELFTWLDQNK 601  
481 CDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLNLYFELFTWLDQNK 540  
602 SFVGMSTDSPPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 661  
541 SFVGMSTDSPPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 600  
662 MILFGEDVRVANLKRISNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDNS 721  
601 MILFGEDVRVANLKRISNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDNS 660  
722 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIIVGVILIFTGIRDKK 770  
661 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIIVGVILIFTGIRDKK 709

RESULT 8  
US-10-158-825-138  
; Sequence 138, Application US/10158825  
; Publication No. US20030138894A1  
; GENERAL INFORMATION:  
; APPLICANT: Tom Parry et al.  
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity  
; FILE REFERENCE: PF555  
; CURRENT APPLICATION NUMBER: US/10/158,825  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 60/294,976  
; PRIOR FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 158  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 138  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (219)..  
; OTHER INFORMATION: Xaa equals any amino acid  
; FEATURE:

NAME/KEY: MISC FEATURE  
LOCATION: (240)...(240)  
FEATURE:  
OTHER INFORMATION: Xaa equals any amino acid  
NAME/KEY: MISC FEATURE  
LOCATION: (499)...(499)  
OTHER INFORMATION: Xaa equals any amino acid  
US-10-158-825-138

Query Match 88.0%; Score 3775; DB 12; Length 711;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 704; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 62 MNNAGDKWGAFLKEQSTLAQMYPLQEIQNLTIVKQLQALQONGSSVLSSEKSKRLNTILN 121  
DB 1 MNNAGDKWGAFLKEQSTLAQMYPLQEIQNLTIVKQLQALQONGSSVLSSEKSKRLNTILN 60  
QY 122 TMSITYSTGKVCNPNPQECLELLEPGLNEIMANSIDYNERLWAWESWSEVKGQRLPYE 181  
DB 61 TMSITYSTGKVCNPNPQECLELLEPGLNEIMANSIDYNERLWAWESWSEVKGQRLPYE 120  
QY 182 EYVVLKNEARAHNYEDYDYNRGDYEYVNGVDGYDSRGQLEDVEHTFEEIKPLYEHLH 241  
DB 121 EYVVLKNEARAHNYEDYDYNRGDYEYVNGVDGYDSRGQLEDVEHTFEEIKPLYEHLH 180  
QY 242 AYVRKLMNAYPSYISPIGCLPAHLGDMWGRFTNLYSLTPVFGQKNIDVTDAVDQA 301  
DB 181 AYVRKLMNAYPSYISPIGCLPAHLGDMWGRFTNLYSLTPVFGQKNIDVTDAVDQX 240  
QY 302 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKDFRILMC 361  
DB 241 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKDFRILMC 300  
QY 362 TKVTMDDFLTAHHEMGHIQYDMAYAAQPPFLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421  
DB 301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPPFLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360  
QY 422 GLSPDFQEDNETEINFLKQALTIIVGTLPTFTYMLEKRWMMVFKGEIPKQDQWKKWEMK 481  
DB 361 GLSPDFQEDNETEINFLKQALTIIVGTLPTFTYMLEKRWMMVFKGEIPKQDQWKKWEMK 420  
QY 482 REIVGVVPEVPHDETYCDPASLPHVSNDSYFIRYTRTLTYQFQOQALCOAAKHGGLPHK 541  
DB 421 REIVGVVPEVPHDETYCDPASLPHVSNDSYFIRYTRTLTYQFQOQALCOAAKHGGLPHK 480  
QY 542 CDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKMNVRLNLYFEPLFTWLKDQKN 601  
DB 481 CDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKMNVRLNLYFEPLFTWLKDQKN 540  
QY 602 SFVGSWTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 661  
DB 541 SFVGSWTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 600  
QY 662 MILFGEDVRVANLKPRISENFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDS 721  
DB 601 MILFGEDVRVANLKPRISENFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDS 660  
QY 722 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIVVGVIVILIFTGIRDRKK 770  
DB 661 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIVVGVIVILIFTGIRDRKK 709

RESULT 9  
US-10-158-847-138  
Sequence 138, Application US/10158847  
Publication No. US20030091557A1  
GENERAL INFORMATION:  
APPLICANT: Tom Parry et al.  
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity  
FILE REFERENCE: PF557  
CURRENT APPLICATION NUMBER: US/10/158,847  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: 60/295,004

PRIOR FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 158  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 138  
LENGTH: 711  
TYPE: PRT  
ORGANISM: homo sapiens  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (219)...(219)  
OTHER INFORMATION: Xaa equals any amino acid  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (240)...(240)  
OTHER INFORMATION: Xaa equals any amino acid  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (499)...(499)  
OTHER INFORMATION: Xaa equals any amino acid  
US-10-158-847-138

Query Match 88.0%; Score 3775; DB 15; Length 711;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 704; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 62 MNNAGDKWGAFLKEQSTLAQMYPLQEIQNLTIVKQLQALQONGSSVLSSEKSKRLNTILN 121  
DB 1 MNNAGDKWGAFLKEQSTLAQMYPLQEIQNLTIVKQLQALQONGSSVLSSEKSKRLNTILN 60  
QY 122 TMSITYSTGKVCNPNPQECLELLEPGLNEIMANSIDYNERLWAWESWSEVKGQRLPYE 181  
DB 61 TMSITYSTGKVCNPNPQECLELLEPGLNEIMANSIDYNERLWAWESWSEVKGQRLPYE 120  
QY 182 EYVVLKNEARAHNYEDYDYNRGDYEYVNGVDGYDSRGQLEDVEHTFEEIKPLYEHLH 241  
DB 121 EYVVLKNEARAHNYEDYDYNRGDYEYVNGVDGYDSRGQLEDVEHTFEEIKPLYEHLH 180  
QY 242 AYVRKLMNAYPSYISPIGCLPAHLGDMWGRFTNLYSLTPVFGQKNIDVTDAVDQA 301  
DB 181 AYVRKLMNAYPSYISPIGCLPAHLGDMWGRFTNLYSLTPVFGQKNIDVTDAVDQX 240  
QY 302 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKDFRILMC 361  
DB 241 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKDFRILMC 300  
QY 362 TKVTMDDFLTAHHEMGHIQYDMAYAAQPPFLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421  
DB 301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPPFLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360  
QY 422 GLSPDFQEDNETEINFLKQALTIIVGTLPTFTYMLEKRWMMVFKGEIPKQDQWKKWEMK 481  
DB 361 GLSPDFQEDNETEINFLKQALTIIVGTLPTFTYMLEKRWMMVFKGEIPKQDQWKKWEMK 420  
QY 482 REIVGVVPEVPHDETYCDPASLPHVSNDSYFIRYTRTLTYQFQOQALCOAAKHGGLPHK 541  
DB 421 REIVGVVPEVPHDETYCDPASLPHVSNDSYFIRYTRTLTYQFQOQALCOAAKHGGLPHK 480  
QY 542 CDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKMNVRLNLYFEPLFTWLKDQKN 601  
DB 481 CDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKMNVRLNLYFEPLFTWLKDQKN 540  
QY 602 SFVGSWTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 661  
DB 541 SFVGSWTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 600  
QY 662 MILFGEDVRVANLKPRISENFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDS 721  
DB 601 MILFGEDVRVANLKPRISENFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDS 660  
QY 722 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIVVGVIVILIFTGIRDRKK 770  
DB 661 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIVVGVIVILIFTGIRDRKK 709

RESULT 10  
US-09-969-384-25  
; Sequence 25, Application US/09969384  
; Publication No. US20020192749A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore, et al.  
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies  
; FILE REFERENCE: PT055P1  
; CURRENT APPLICATION NUMBER: US/09/969,384  
; PRIOR FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: PCT/US01/10542  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: 60/236,384  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/194,118  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 681  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (219)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (240)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (499)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-969-384-25  
Query Match 84.9%; Score 3643; DB 10; Length 681;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 676; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 62 MNNAGDKWSAFLEKQSTLAQMPLOEIQNLTVKLOLQALQOQSSVLSDEKSKRLNTILN 121  
Db 1 MNNAGDKWSAFLEKQSTLAQMPLOEIQNLTVKLOLQALQOQSSVLSDEKSKRLNTILN 60  
Qy 122 TMSTIYTGKVCNPDNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181  
Db 61 TMSTIYTGKVCNPDNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120  
Qy 182 EYVVLKNEARAHNYEDYDGYWRGDIYVNGVDYSGQLIEDVEHTFEEIKPLYEHLH 241  
Db 121 EYVVLKNEARAHNYEDYDGYWRGDIYVNGVDYSGQLIEDVEHTFEEIKPLYEHLH 180  
Qy 242 AYVRKLMNAYPSYISPIGCLPAHLGDMGGRFNTNLYSLTVPFQKPNIDVTDAMVDQA 301  
Db 181 AYVRKLMNAYPSYISPIGCLPAHLGDMGGRFNTNLYSLTVPFQKPNIDVTDAMVDQA 240  
Qy 302 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLMC 361  
Db 241 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLMC 300  
Qy 362 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421  
Db 301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360  
Qy 422 GLLSPDFQEDNETEINFLKQALITVGLTPPTYMLEKRWVFKGEIPKQWKKWEMK 481  
Db 361 GLLSPDFQEDNETEINFLKQALITVGLTPPTYMLEKRWVFKGEIPKQWKKWEMK 420  
Qy 482 REIVGVVEPVPHDETCDPASLPHVSNDSYFIRYITRTLYQFQOEALCOAAKHEGGLHK 541  
Db 421 REIVGVVEPVPHDETCDPASLPHVSNDSYFIRYITRTLYQFQOEALCOAAKHEGGLHK 480  
Qy 542 CDISNSTEAGOKLFNMLRKXKSEPTWLTALENVGAKNNVRPILNYPEPLFTWLKDQKN 601

Db 481 CDISNSTEAGOKLFNMLRKXKSEPTWLTALENVGAKNNVRPILNYPEPLFTWLKDQKN 540  
Qy 602 SFVGWSTDMSPYADQSIKVRISLKSALGDKAYENNDNMYLFRSSVAYAMRQYPLKYNQ 661  
Db 541 SFVGWSTDMSPYADQSIKVRISLKSALGDKAYENNDNMYLFRSSVAYAMRQYPLKYNQ 600  
Qy 662 MILGGEEDVRANUKPRISNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLDNS 721  
Db 601 MILGGEEDVRANUKPRISNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLDNS 660  
Qy 722 LEFLGIQPTLGLPPNPQPPVSIW 742  
Db 661 LEFLGIQPTLGLPPNPQPPVSIW 681  
RESULT 11  
US-10-158-825-140  
; Sequence 140, Application US/10158825  
; Publication No. US20030138894A1  
; GENERAL INFORMATION:  
; APPLICANT: Tom Parry et al.  
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity  
; FILE REFERENCE: PFS55  
; CURRENT APPLICATION NUMBER: US/10/158,825  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 60/294,976  
; PRIOR FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 158  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 140  
; LENGTH: 681  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (219)-(219)  
; OTHER INFORMATION: Xaa equals any amino acid  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (240)-(240)  
; OTHER INFORMATION: Xaa equals any amino acid  
; NAME/KEY: MISC FEATURE  
; LOCATION: (499)-(499)  
; OTHER INFORMATION: Xaa equals any amino acid  
US-10-158-825-140  
Query Match 84.9%; Score 3643; DB 12; Length 681;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 676; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 62 MNNAGDKWSAFLEKQSTLAQMPLOEIQNLTVKLOLQALQOQSSVLSDEKSKRLNTILN 121  
Db 1 MNNAGDKWSAFLEKQSTLAQMPLOEIQNLTVKLOLQALQOQSSVLSDEKSKRLNTILN 60  
Qy 122 TMSTIYTGKVCNPDNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181  
Db 61 TMSTIYTGKVCNPDNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120  
Qy 182 EYVVLKNEARAHNYEDYDGYWRGDIYVNGVDYSGQLIEDVEHTFEEIKPLYEHLH 241  
Db 121 EYVVLKNEARAHNYEDYDGYWRGDIYVNGVDYSGQLIEDVEHTFEEIKPLYEHLH 180  
Qy 242 AYVRKLMNAYPSYISPIGCLPAHLGDMGGRFNTNLYSLTVPFQKPNIDVTDAMVDQA 301  
Db 181 AYVRKLMNAYPSYISPIGCLPAHLGDMGGRFNTNLYSLTVPFQKPNIDVTDAMVDQA 240  
Qy 302 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLMC 361  
Db 241 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLMC 300  
Qy 362 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421

Db	301	TKVTWDDFLTAHHEMCHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI	360
Qy	422	GLLSPDFQEDNETEINFLLKQALITVGLPPTYMLEKRWVFKGEIPKQOMKQWEMK	481
Db	361	GLLSPDFQEDNETEINFLLKQALITVGLPPTYMLEKRWVFKGEIPKQOMKQWEMK	420
Qy	482	REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTYLQFQOEALCQAAKHEGFLHK	541
Db	421	REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTYLQFQOEALCQAAKHEGFLHK	480
Qy	542	CDISNSTEAGOKLFNMLRGKSEPWTLALENVVGAKNVRLPILNYPEPLFTWLKQONKN	601
Db	481	CDISNSTEAGOKLFNMLRGKSEPWTLALENVVGAKNVRLPILNYPEPLFTWLKQONKN	540
Qy	602	SVFGWSTDWSPVADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMQYFLKVKNQ	661
Db	541	SVFGWSTDWSPVADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMQYFLKVKNQ	600
Qy	662	MILFGEEDVRVANLKPRISEFNFVFTAPKNVSDIIPRTEVEKAIRMSRINDAFRLNDS	721
Db	601	MILFGEEDVRVANLKPRISEFNFVFTAPKNVSDIIPRTEVEKAIRMSRINDAFRLNDS	660
Qy	722	LEFLGIQPTLGPPOPPVSIW 742	
Db	661	LEFLGIQPTLGPPOPPVSIW 681	
RESULT 12			
US-10-158-847-140			
; Sequence 140, Application US/10158847			
; Publication No. US20030091557A1			
; GENERAL INFORMATION:			
; APPLICANT: Tom Parry et al.			
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity			
; FILE REFERENCE: PF557			
; CURRENT APPLICATION NUMBER: US/10/158,847			
; PRIOR FILING DATE: 2002-06-03			
; PRIOR APPLICATION NUMBER: 60/295,004			
; PRIOR FILING DATE: 2001-06-04			
; NUMBER OF SEQ ID NOS: 158			
; SOFTWARE: Patent in version 3.1			
; SEQ ID NO 140			
; LENGTH: 681			
; TYPE: PRT			
; ORGANISM: homo sapiens			
; FEATURE:			
; NAME/KEY: MISC FEATURE			
; LOCATION: (219)..(219)			
; OTHER INFORMATION: Xaa equals any amino acid			
; FEATURE:			
; NAME/KEY: MISC FEATURE			
; LOCATION: (240)..(240)			
; OTHER INFORMATION: Xaa equals any amino acid			
; FEATURE:			
; NAME/KEY: MISC FEATURE			
; LOCATION: (499)..(499)			
; OTHER INFORMATION: Xaa equals any amino acid			
US-10-158-847-140			
Query Match 84.9%; Score 3643; DB 15; Length 681;			
Best Local Similarity 99.3%; Pred. No. 0;			
Matches 676; Conservative 1; Mismatches 4; Indels 0; Gaps 0;			
Qy	62	MNNAAGDKSAFLKEQSTLAQMPLOEQITONITVKLQALQONGSSVLSDKSKRLNTILN	121
Db	1	MNNAAGDKSAFLKEQSTLAQMPLOEQITONITVKLQALQONGSSVLSDKSKRLNTILN	60
Qy	122	TMSIYSTGKVCNPDNPOECCLLPGLNEIWMANSLDYNRLWAWESRSEVQKOLRPLYE	181
Db	61	TMSIYSTGKVCNPDNPOECCLLPGLNEIWMANSLDYNRLWAWESRSEVQKOLRPLYE	120
Qy	182	EYVVLKQEMARAHYEDYDGYWRGDYEVNGVDYISRGQLIEDVEHTFEIKPLYEHLH	241

Db	121	EYVVLKQEMARAHYEDYDGYWRGDYEVNGVDYISRGQLIEDVEHTFEIKPLYEHLH	180
Qy	242	AVVRAKLAMNAPSYISPIGCLPAHLGDMWGRFMTNLYSLTVPPGQKPNIDVTAMVDOA	301
Db	181	AVVRAKLAMNAPSYISPIGCLPAHLGDMWGRFMTNLYSLTVPPGQKPNIDVTAMVDOX	240
Qy	302	WDAQRIFKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTANDLGKDFRILWC	361
Db	241	WDAQRIFKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTANDLGKDFRILMC	300
Qy	362	TKVTWDDFLTAHHEMCHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI	421
Db	301	TKVTWDDFLTAHHEMCHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI	360
Qy	422	GLLSPDFQEDNETEINFLLKQALITVGLPPTYMLEKRWVFKGEIPKQOMKQWEMK	481
Db	361	GLLSPDFQEDNETEINFLLKQALITVGLPPTYMLEKRWVFKGEIPKQOMKQWEMK	420
Qy	482	REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTYLQFQOEALCQAAKHEGFLHK	541
Db	421	REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTYLQFQOEALCQAAKHEGFLHK	480
Qy	542	CDISNSTEAGOKLFNMLRGKSEPWTLALENVVGAKNVRLPILNYPEPLFTWLKQONKN	601
Db	481	CDISNSTEAGOKLFNMLRGKSEPWTLALENVVGAKNVRLPILNYPEPLFTWLKQONKN	540
Qy	602	SVFGWSTDWSPVADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMQYFLKVKNQ	661
Db	541	SVFGWSTDWSPVADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMQYFLKVKNQ	600
Qy	662	MILFGEEDVRVANLKPRISEFNFVFTAPKNVSDIIPRTEVEKAIRMSRINDAFRLNDS	721
Db	601	MILFGEEDVRVANLKPRISEFNFVFTAPKNVSDIIPRTEVEKAIRMSRINDAFRLNDS	660
Qy	722	LEFLGIQPTLGPPOPPVSIW 742	
Db	661	LEFLGIQPTLGPPOPPVSIW 681	
RESULT 13			
US-09-978-385-6			
; Sequence 6, Application US/09978385			
; Patent No. US20020177211A1			
; GENERAL INFORMATION:			
; APPLICANT: Piddington, Christopher S.			
; APPLICANT: Petrie, Charles			
; APPLICANT: Shoemaker, Kimberly E.			
; APPLICANT: Bishop, Paul D.			
; TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME			
; FILE REFERENCE: 99-24C1			
; CURRENT APPLICATION NUMBER: US/09/978,385			
; CURRENT FILING DATE: 2001-10-16			
; PRIOR APPLICATION NUMBER: 60/133,952			
; PRIOR FILING DATE: 1999-05-13			
; PRIOR APPLICATION NUMBER: 60/151,181			
; PRIOR FILING DATE: 1999-08-27			
; PRIOR APPLICATION NUMBER: 09/563,516			
; PRIOR FILING DATE: 2000-05-03			
; NUMBER OF SEQ ID NOS: 11			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 6			
; LENGTH: 805			
; TYPE: PRT			
; ORGANISM: Mouse			
US-09-978-385-6			
Query Match 83.4%; Score 3579; DB 10; Length 805;			
Best Local Similarity 82.1%; Pred. No. 0;			
Matches 661; Conservative 60; Mismatches 84; Indels 0; Gaps 0;			
Qy	1	MSSSWLLLSLVAVTAQAQSTIEQAQKFLDKFNHEADLFYQSSLASWNTNTITEENVQ	60
Db	1	MSSSWLLLSLVAVTTAQSLEENAKTFLNNFNQEAEDLSYQSSLASWNTNTITEENQA	60



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Qy 61 NMNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQOQSSVLSEDKSRINTIL 120
Db 61 KMSEAAKWSAFYEQSKTAQSFSLQEIQTPIIKRQALQOQSSGSSALSADKNKQNTIL 120
Qy 121 NTMSTIYSTGKVCNPNQPCQLLEPGLNEIMANSLDYNERLWAWESRSEVKGQLRPLY 180
Db 121 NTMSTIYSTGKVCNPNQPCQLLEPGLDEIMATSTDYNSRLWAWEGRAEVKGQLRPLY 180
Qy 181 EBYVVLKNEMARANHYEDYDYGWGDYEVNGVDYDYSRGQIEDVEHTFEEIKPLYEHL 240
Db 181 EBYVVLKNEMARANNYDYGWGDYEAAGDGYNNENQLIEDVERTFAEIKPLYEHL 240
Qy 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMWGFNTNLXSLTVFPQKPNIDVTDAMVQ 300
Db 241 HAYVRRKLMNTYPSYISPTGCLPAHLGDMWGFNTNLXSLTVFPQKPNIDVTDAMNQ 300
Qy 301 AWDAORIFKEAEKPFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRIIM 360
Db 301 GWAERIFQEAERKFVSVGLPHTQGFWNSMLTEPADGRKVVCHPTAWDLGHGDFRIIM 360
Qy 361 CTKVMTDDFLTAAHEMIGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
Db 361 CTKVMTDNFLTAAHEMIGHIQYDMAYARQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
Qy 421 IGLLSPDFQEDNETEINFLLKQALTIIVGTLPTFTYMLEKRWMMVFKEI PKQOMWKWEM 480
Db 421 IGLLSPDFQEDSETEINFLLKQALTIIVGTLPTFTYMLEKRWMMVFGEI PKQOMWKWEM 480
Qy 481 KREIVGVVPEVPHDTEYCDPASLFHVSNDYSFIRYTRTYQFQFQALCOAAKHEGPHL 540
Db 481 KREIVGVVPELPHDTEYCDPASLFHVSNDYSFIRYTRTYQFQFQALCOAAKNGSLH 540
Qy 541 KCDISNSTEAGQKLFNMLRGKSEPTWTLALENVVGAQNMVRLNLYFPLFTWLKQNK 600
Db 541 KCDISNSTEAGQKLLKMLSLGNSEPTWTKALENVVGAENMDVKPLNLYFQPLFDMKEQNR 600
Qy 601 NSFVGMSTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVKY 660
Db 601 NSFVGMNTWSPYADQSIKVRISLSKALGANAYEWNTNEMFLFRSSVAYAMRYFIIKN 660
Qy 661 QMILFGBEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720
Db 661 QTVPFLEEDVRVSDLKPRVSFYFVTSPQNVSDVPRSEVEDAIRMSGRINDVFGIND 720
Qy 721 SLEFLGIQPLTPNQPVSIMLIVGVVMGVIVGIVILIFTGIRDRKKKKKARSGENP 780
Db 721 SLEFLGIHTLEPPYQPPVTIWLIFGVVMALVVVGIILIVTGIKGRKKKNETKREENP 780
Qy 781 YASIDISKGENNPGFQNTDDVQTSF 805
Db 781 YDSMDIGKESNAGFQNSDDAQTsf 805
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## RESULT 14

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US-09-978-385-9
; Sequence 9, Application US/09978385
; Patent No. US20020177211A1
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Petrie, Charles
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
; FILE REFERENCE: 99-24C1
; CURRENT APPLICATION NUMBER: US/09/978,385
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/133,952
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/151,181
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/563,516
```

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Mouse
US-09-978-385-9
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Query Match 83.0%; Score 3561; DB 10; Length 805;
Best Local Similarity 81.9%; Pred. No. 7,3e-317;
Matches 559; Conservative 60; Mismatches 86; Indels 0; Gaps 0;
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Qy 1 MSSSSWLLLSLVATAAQSTIEEOAKTFLDKFHEAEDLIFYOSSLASWNTNTITEENVQ 60
Db 1 MSSSSWLLLSLVATAAQSTIEENAKTFLANNFNOEADLSYQSSLASWNTNTITEENAQ 60
Qy 61 NMNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQOQSSVLSEDKSRINTIL 120
Db 61 KMSEAAKWSAFYEQSKTAQSFSLQEIQTPIIKRQALQOQSSGSSALSADKNKQNTIL 120
Qy 121 NTMSTIYSTGKVCNPNQPCQLLEPGLNEIMANSLDYNERLWAWESRSEVKGQLRPLY 180
Db 121 NTMSTIYSTGKVCNPNQPCQLLEPGLDEIMATSTDYNSRLWAWEGRAEVKGQLRPLY 180
Qy 181 EBYVVLKNEMARANHYEDYDYGWGDYEVNGVDYDYSRGQIEDVEHTFEEIKPLYEHL 240
Db 181 EBYVVLKNEMARANNYDYGWGDYEAAGDGYNNENQLIEDVERTFAEIKPLYEHL 240
Qy 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMWGFNTNLXSLTVFPQKPNIDVTDAMVQ 300
Db 241 HAYVRRKLMNTYPSYISPTGCLPAHLGDMWGFNTNLXSLTVFPQKPNIDVTDAMNQ 300
Qy 301 AWDAORIFKEAEKPFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRIIM 360
Db 301 GWAERIFQEAERKFVSVGLPHTQGFWNSMLTEPADGRKVVCHPTAWDLGHGDFRIIM 360
Qy 361 CTKVMTDDFLTAAHEMIGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
Db 361 CTKVMTDNFLTAAHEMIGHIQYDMAYARQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
Qy 421 IGLLSPDFQEDNETEINFLLKQALTIIVGTLPTFTYMLEKRWMMVFKEI PKQOMWKWEM 480
Db 421 IGLLSPDFQEDSETEINFLLKQALTIIVGTLPTFTYMLEKRWMMVFGEI PKQOMWKWEM 480
Qy 481 KREIVGVVPEVPHDTEYCDPASLFHVSNDYSFIRYTRTYQFQFQALCOAAKHEGPHL 540
Db 481 KREIVGVVPELPHDTEYCDPASLFHVSNDYSFIRYTRTYQFQFQALCOAAKNGSLH 540
Qy 541 KCDISNSTEAGQKLFNMLRGKSEPTWTLALENVVGAQNMVRLNLYFPLFTWLKQNK 600
Db 541 KCDISNSTEAGQKLLKMLSLGNSEPTWTKALENVVGAENMDVKPLNLYFQPLFDMKEQNR 600
Qy 601 NSFVGMSTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVKY 660
Db 601 NSFVGMNTWSPYADQSIKVRISLSKALGANAYEWNTNEMFLFRSSVAYAMRYFIIKN 660
Qy 661 QMILFGBEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720
Db 661 QTVPFLEEDVRVSDLKPRVSFYFVTSPQNVSDVPRSEVEDAIRMSGRINDVFGIND 720
Qy 721 SLEFLGIQPLTPNQPVSIMLIVGVVMGVIVGIVILIFTGIRDRKKKKKARSGENP 780
Db 721 SLEFLGIHTLEPPYQPPVTIWLIFGVVMALVVVGIILIVTGIKGRKKKNETKREENP 780
Qy 781 YASIDISKGENNPGFQNTDDVQTSF 805
Db 781 YDSMDIGKESNAGFQNSDDAQTsf 805
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## RESULT 15

```
US-10-137-870-72
; Sequence 72, Application US/10137870
; Publication No. US2003013883A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC155
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 72
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-72

Query Match          69.4%; Score 2979; DB 12; Length 555;
Best Local Similarity 99.8%; Pred. No. 8.6e-264;
Matches 553; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFDKFNHEAEADLFYQSSLASWNTNTNTEENVQ 60
DB 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFDKFNHEAEADLFYQSSLASWNTNTNTEENVQ 60
QY 61 NNNNAGDKWSAFLEKQSTLAQMYPLQEIQNTLVKLQALQONGSSVLSEDKSKRLNTIL 120
DB 61 NNNNAGDKWSAFLEKQSTLAQMYPLQEIQNTLVKLQALQONGSSVLSEDKSKRLNTIL 120
QY 121 NTMSTIYSTGKVCNPDNPOECILLBPLGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
DB 121 NTMSTIYSTGKVCNPDNPOECILLBPLGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
QY 181 EYVVLKNEWARANHYEDYDWRGDYVNGDYVNGDYVNGDYVNGDYVNGDYVNGDYVNGDYV 240
DB 181 EYVVLKNEWARANHYEDYDWRGDYVNGDYVNGDYVNGDYVNGDYVNGDYVNGDYVNGDYV 240
QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLGLDMGGRFWTNLYSLTVPGQKPNIDVTDAMVDQ 300
DB 241 HAYVRAKLMNAYPSYISPIGCLPAHLGLDMGGRFWTNLYSLTVPGQKPNIDVTDAMVDQ 300
QY 301 AMDAQRI FKEAEKFVSVGLPNNTOGFWNSMLTDPGNVQKAVCHPTAWDLKGDFFRLM 360
DB 301 AMDAQRI FKEAEKFVSVGLPNNTOGFWNSMLTDPGNVQKAVCHPTAWDLKGDFFRLM 360
QY 361 CTKVTWDDFLTAHHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
DB 361 CTKVTWDDFLTAHHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
QY 421 IGLSPDFQEDNETEINFLKQALTIIVGLTPFTYMLEKRWVWFKEI PKDQWKKWEM 480
DB 421 IGLSPDFQEDNETEINFLKQALTIIVGLTPFTYMLEKRWVWFKEI PKDQWKKWEM 480
QY 481 KREIVGVFVPVPHDEYCDPASLFHVSNDYSFIRYVTRTYLQFQEQALCQAAKHEGPLH 540
DB 481 KREIVGVFVPVPHDEYCDPASLFHVSNDYSFIRYVTRTYLQFQEQALCQAAKHEGPLH 540
QY 541 KCDISNSTEAGQKL 554

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Db 541 KCDISNSTEAGQKL 554

Search completed: February 19, 2004, 19:53:06  
Job time : 42 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2004, 19:47:18 ; Search time 41 Seconds  
(without alignments)

5066.643 Million cell updates/sec

Title: US-09-163-648-2

Perfect score: 4291

Sequence: 1 MSSSWLLSLVAVTAAGT.....ISKGNPQFQNTDDVQTSF 805

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phage:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_rvirus:
- 16: sp\_bacteriap:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4291	100.0	805	4 Q9NRA7	Q9nra7 homo sapien
2	4288	99.9	805	4 Q9BYF1	Q9byf1 homo sapien
3	4281	99.8	804	4 Q9UFZ6	Q9ufz6 homo sapien
4	3579	83.4	805	11 Q8R010	Q8r010 mus musculus
5	3485	81.2	798	11 Q9N971	Q9n971 mus musculus
6	1539	35.9	353	11 Q9N970	Q9n970 mus musculus
7	1347.5	31.4	739	4 Q9N710	Q9n710 homo sapien
8	1336	31.1	732	6 Q9GLN6	Q9glne pan troglod
9	1334	31.1	1015	11 Q8K233	Q8k233 mus musculus
10	1329	31.0	1304	6 Q9GLN7	Q9glne pan troglod
11	1310	30.5	775	11 Q8CLN1	Q8cln1 rattus norv
12	1310	30.5	1313	11 Q9ECM9	Q9ecm9 rattus norv
13	1303	30.4	694	4 Q15540	Q15540 homo sapien
14	1100.5	25.6	619	16 Q8EE93	Q8ee93 shewanella
15	1089.5	25.4	648	5 Q9NDS8	Q9nds8 bombyx mori
16	1071	25.0	265	11 Q9D836	Q9d836 mus musculus

## ALIGNMENTS

### RESULT 1

ID	Q9NRA7	PRELIMINARY;	PRT;	805 AA.
AC	Q9NRA7;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Angiotensin converting enzyme-like protein (ACE-related carboxypeptidase ACE2).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymphona;			
RA	Tipnis S.R.; Hooper N.M.; Hyde R.J.; Christie G.; Karran E.,			
RA	Turner A.J.;			
RT	"A Human Homolog of Angiotensin Converting Enzyme - Cloning and Functional Expression As A Captopril-Insensitive Carboxypeptidase."			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Donoghue M., Hsieh F., Baronas E., Godbout K., Gosselin M.,			
RA	Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,			
RA	Breitbart R.E.; Acton S.;			
RT	"A novel ACE-related carboxypeptidase (ACE2) converts angiotensin I to angiotensin1-9."			
RL	Circ. Res. 0:0-0(2000).			
DR	EMBL; AF241254; AAF78220.1; --			
DR	EMBL; AF291820; AAF99721.1; --			
DR	MEROPS; M02.006; --			
DR	InterPro; IPR001548; Peptidase_M2.			
DR	InterPro; IPR006025; Zn_Mtpetdse.			
DR	Pfam; PF01401; Peptidase_M2; 1.			
DR	PRINTS; PR00791; PEPDPTASEA.			
DR	ProDom; PD004184; Peptidase_M2; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.			
KW	Carboxypeptidase.			

17	1057	24.6	660	5	Q17248
18	1030	24.0	630	5	Q24222
19	1028	24.0	630	5	Q9VLJ6
20	968.5	22.6	672	16	Q8PN56
21	967	22.5	672	16	Q8PBK3
22	930	21.7	844	5	Q8SXX2
23	737	17.2	674	5	Q9VJV1
24	641	14.9	906	5	Q18581
25	500.5	11.7	609	5	Q9V520
26	500.5	11.7	620	5	Q8MS05
27	476	11.1	611	5	Q9VJV2
28	434.5	10.1	202	11	Q64603
29	409.5	9.5	628	5	Q9M021
30	408.5	9.5	628	5	Q9SUS9
31	390	9.1	222	11	Q9ESG3
32	387	9.0	222	4	Q9HBJ8
33	386	9.0	222	11	Q9ESG4
34	306.5	7.1	121	6	Q9BDG1
35	280.5	6.5	135	4	Q16425
36	251.5	5.9	157	11	Q61265
37	171.5	4.0	154	5	Q8IP60
38	157	3.7	532	16	Q9KPV0
39	154	3.6	502	16	Q8Y616
40	152.5	3.6	734	5	Q9NKE3
41	147	3.4	54	6	Q95161
42	147	3.4	502	16	Q92AC3
43	139.5	3.3	987	16	Q8YWG6
44	139	3.2	608	16	Q9PR80
45	138.5	3.2	613	16	Q8D8J9

Q17248 boophilus m  
Q24222 drosophila  
Q9VLJ6 drosophila  
Q8PN56 xanthomonas  
Q8PBK3 xanthomonas  
Q8SXX2 drosophila  
Q9VJV1 drosophila  
Q18581 caenorhabdi  
Q9V520 drosophila  
Q8MS05 drosophila  
Q9VJV2 drosophila  
Q64603 rattus norv  
Q9M021 drosophila  
Q9SUS9 drosophila  
Q9ESG3 rattus norv  
Q9HBJ8 homo sapien  
Q9ESG4 mus musculu  
Q9BDG1 bos taurus  
Q16425 homo sapien  
Q61265 mus musculu  
Q8IP60 drosophila  
Q8KPV0 bacillus ha  
Q8Y616 listeria mo  
Q9NKE3 drosophila  
Q95161 canis fami  
Q92AC3 listeria in  
Q8YWG6 anabaena sp  
Q9PR80 ureaplasma  
Q8D8J9 vibrio vuln

SQ SEQUENCE 805 AA; 92462 MW; 8BE6E0A93155058 CRC64;  
Query Match 100.0%; Score 4291; DB 4; Length 805;  
Best Local Similarity 100.0%; Pred. No. 1.4e-308;  
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSSSWLLSLVAVTAQAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60  
DB 1 MSSSWLLSLVAVTAQAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60  
QY 61 NMNAGDKWSAFLEQSTLAQMYPLOEIQNLTKVLQALQONGSSVLSDEKSKRLNTIL 120  
DB 61 NMNAGDKWSAFLEQSTLAQMYPLOEIQNLTKVLQALQONGSSVLSDEKSKRLNTIL 120  
QY 121 NTMTSTIYGTGKVCNPNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVKGQRLPLY 180  
DB 121 NTMTSTIYGTGKVCNPNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVKGQRLPLY 180  
QY 181 EYVVLKNEMARANHVEDYGDYWRGDEYVNGVDYDYSRGQLIEDVEHTFEIKPLYEHL 240  
DB 181 EYVVLKNEMARANHVEDYGDYWRGDEYVNGVDYDYSRGQLIEDVEHTFEIKPLYEHL 240  
QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMGWFNLTYSITVFPQKPNIDVTDAWVQ 300  
DB 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMGWFNLTYSITVFPQKPNIDVTDAWVQ 300  
QY 301 AWAQRIKFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLM 360  
DB 301 AWAQRIKFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLM 360  
QY 361 CTKVTMDPFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
DB 361 CTKVTMDPFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
QY 421 IGLSPDFQEDNETEINFLLKQALTIYVGLPFTYMLEKRWMMVFKEIPKQWKKWEM 480  
DB 421 IGLSPDFQEDNETEINFLLKQALTIYVGLPFTYMLEKRWMMVFKEIPKQWKKWEM 480  
QY 481 KREIVGVVEVPVPHDETYCDPASLFHVSNDYSFIRYTRTLTLYQFQOEALCOAAKHEGPH 540  
DB 481 KREIVGVVEVPVPHDETYCDPASLFHVSNDYSFIRYTRTLTLYQFQOEALCOAAKHEGPH 540  
QY 541 KCDISNSTEAGQKLFNMLRGKSEPTLALENVGAKNMNVRPLNYPFLFTWLKDQNK 600  
DB 541 KCDISNSTEAGQKLFNMLRGKSEPTLALENVGAKNMNVRPLNYPFLFTWLKDQNK 600  
QY 601 NSFVGSWTDSPYADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKYN 660  
DB 601 NSFVGSWTDSPYADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKYN 660  
QY 661 QMILFGEEDVRVANLKPRISEFPFTAPKNVSDIIPRTEVEKAIIRMSRSRINDAFLNDN 720  
DB 661 QMILFGEEDVRVANLKPRISEFPFTAPKNVSDIIPRTEVEKAIIRMSRSRINDAFLNDN 720  
QY 721 SLEFLGIQPTLGPNNOPPSYIMLIVFGVVMGVIWGVIVILFTGIRDRKKKNGKARSGENP 780  
DB 721 SLEFLGIQPTLGPNNOPPSYIMLIVFGVVMGVIWGVIVILFTGIRDRKKKNGKARSGENP 780  
QY 781 YASIDISKGNPFGONTDDVQTSF 805  
DB 781 YASIDISKGNPFGONTDDVQTSF 805

## RESULT 2

Q9BYF1 PRELIMINARY; PRT; 805 AA.  
ID Q9BYF1  
AC Q9BYF1;  
DT 01-JUN-2001 (TEMBLrel. 17, Created)  
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
GN ACE2.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Komatsu T., Suzuki Y., Sugano S.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Suzuki Y., Watanabe M., Sugano S.;  
RT "Cloning, expression analysis and chromosomal localization of a novel  
RT ACE like enzyme."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB046569; BAB40370.1; --  
DR MEROPS; M02.006; --  
DR Genew; HGNC:13557; ACE2.  
DR InterPro; IPR001548; Peptidase M2.  
DR InterPro; IPR006025; Zn\_Mtpeptidse.  
DR Pfam; PF01401; Peptidase M2; 1.  
DR PRINTS; PR00791; PEPDPTASEA.  
DR ProDom; PD004184; Peptidase M2; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
SQ SEQUENCE 805 AA; 92491 MW; D2AAB4C27088EB72 CRC64;  
Query Match 99.9%; Score 4288; DB 4; Length 805;  
Best Local Similarity 99.9%; Pred. No. 2.4e-308;  
Matches 804; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSSSWLLSLVAVTAQAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60  
DB 1 MSSSWLLSLVAVTAQAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60  
QY 61 NMNAGDKWSAFLEQSTLAQMYPLOEIQNLTKVLQALQONGSSVLSDEKSKRLNTIL 120  
DB 61 NMNAGDKWSAFLEQSTLAQMYPLOEIQNLTKVLQALQONGSSVLSDEKSKRLNTIL 120  
QY 121 NTMTSTIYGTGKVCNPNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVKGQRLPLY 180  
DB 121 NTMTSTIYGTGKVCNPNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVKGQRLPLY 180  
QY 181 EYVVLKNEMARANHVEDYGDYWRGDEYVNGVDYDYSRGQLIEDVEHTFEIKPLYEHL 240  
DB 181 EYVVLKNEMARANHVEDYGDYWRGDEYVNGVDYDYSRGQLIEDVEHTFEIKPLYEHL 240  
QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMGWFNLTYSITVFPQKPNIDVTDAWVQ 300  
DB 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMGWFNLTYSITVFPQKPNIDVTDAWVQ 300  
QY 301 AWAQRIKFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLM 360  
DB 301 AWAQRIKFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLM 360  
QY 361 CTKVTMDPFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
DB 361 CTKVTMDPFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
QY 421 IGLSPDFQEDNETEINFLLKQALTIYVGLPFTYMLEKRWMMVFKEIPKQWKKWEM 480  
DB 421 IGLSPDFQEDNETEINFLLKQALTIYVGLPFTYMLEKRWMMVFKEIPKQWKKWEM 480  
QY 481 KREIVGVVEVPVPHDETYCDPASLFHVSNDYSFIRYTRTLTLYQFQOEALCOAAKHEGPH 540  
DB 481 KREIVGVVEVPVPHDETYCDPASLFHVSNDYSFIRYTRTLTLYQFQOEALCOAAKHEGPH 540  
QY 541 KCDISNSTEAGQKLFNMLRGKSEPTLALENVGAKNMNVRPLNYPFLFTWLKDQNK 600  
DB 541 KCDISNSTEAGQKLFNMLRGKSEPTLALENVGAKNMNVRPLNYPFLFTWLKDQNK 600  
QY 601 NSFVGSWTDSPYADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKYN 660  
DB 601 NSFVGSWTDSPYADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKYN 660  
QY 661 QMILFGEEDVRVANLKPRISEFPFTAPKNVSDIIPRTEVEKAIIRMSRSRINDAFLNDN 720  
DB 661 QMILFGEEDVRVANLKPRISEFPFTAPKNVSDIIPRTEVEKAIIRMSRSRINDAFLNDN 720

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Db 661 QMLFGEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDN 720
Qy 721 SLBFLGIQPTLGPNNQPPVSIWLVGVVGMVIVGIVILITGIRDRKKKAKSGENP 780
Db 721 SLBFLGIQPTLGPNNQPPVSIWLVGVVGMVIVGIVILITGIRDRKKKAKSGENP 780
Qy 781 YASIDISKGENNPGFQNTDDVQTSF 805
Db 781 YASIDISKGENNPGFQNTDDVQTSF 805

RESULT 3
Q9UFZ6 PRELIMINARY; PRT; 804 AA.
ID Q9UFZ6
AC Q9UFZ6
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP434A014.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL110224; CAB53682.1; -.
DR MEROPS; M02.006; -.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Zn_Mtpeptdse.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPDPTASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 804 AA; 92340 MW; 91FF391074CB5DA9 CRC64;

Query Match 99.8%; Score 4281; DB 4; Length 804;
Best Local Similarity 99.9%; Pred. No. 7.9e-308;
Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SSSSWLLLSLVAVTAQAQSTIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQ 61
Db 1 SSSSWLLLSLVAVTAQAQSTIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQ 60
Qy 62 MNAGDKWSAFLEKQSTLAQMYPLQEIQNLTQVQLQALQALQNGSSVLSDEKSKRLNTILN 121
Db 61 MNAGDKWSAFLEKQSTLAQMYPLQEIQNLTQVQLQALQALQNGSSVLSDEKSKRLNTILN 120
Qy 122 TMSTIYTGKVCNPDNPQECILLPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLYE 181
Db 121 TMSTIYTGKVCNPDNPQECILLPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLYE 180
Qy 182 EYVLKNEARANHYEDYDWRGDEYVNGVDYDYSRGQLIEDVEHTFEEIKPLYEHLH 241
Db 181 EYVLKNEARANHYEDYDWRGDEYVNGVDYDYSRGQLIEDVEHTFEEIKPLYEHLH 240
Qy 242 AYVRAKLMNVPYSISPICGLPAHLGDMWGRFTWNLVSLTPVGQKPNIDVTDMYDQA 301
Db 241 AYVRAKLMNVPYSISPICGLPAHLGDMWGRFTWNLVSLTPVGQKPNIDVTDMYDQA 300
Qy 302 WDAQRIFKEAEKFFVSVGLPNWTOGFWNSMLTDPGNVQKAVCHPTADLKGDFRILMC 361
Db 301 WDAQRIFKEAEKFFVSVGLPNWTOGFWNSMLTDPGNVQKAVCHPTADLKGDFRILMC 360
Qy 362 TKVTMDDFLTARHMGHTIQYDMAYAAQPFLLRNGANEGFHAEGEIMSLSAATPKHLKSI 421
Db 361 TKVTMDDFLTARHMGHTIQYDMAYAAQPFLLRNGANEGFHAEGEIMSLSAATPKHLKSI 420
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Qy 422 GLLSPDFQEDNETEINFLKQALTIIVGTLPTFTYMLEKRWVWFKGEIPKQDMKKWEMK 481
Db 421 GLLSPDFQEDNETEINFLKQALTIIVGTLPTFTYMLEKRWVWFKGEIPKQDMKKWEMK 480
Qy 482 REIVGVVEPVPDHDTYCDPASLHFVSNDSYFIRYTYFTLYQFOQOEALCOAAKHEGPLHK 541
Db 481 REIVGVVEPVPDHDTYCDPASLHFVSNDSYFIRYTYFTLYQFOQOEALCOAAKHEGPLHK 540
Qy 542 CDISNSTEAGOKLFNMLRLGKSEPTWTLALENVVGAKNNVRPLNLYFEPLFTWLKDQKN 601
Db 541 CDISNSTEAGOKLFNMLRLGKSEPTWTLALENVVGAKNNVRPLNLYFEPLFTWLKDQKN 600
Qy 602 SFVGNSTDWSPYADQSKVIRISLSKALGDKAYENDNEMYLFRSSVAYANROYELKVKNQ 661
Db 601 SFVGNSTDWSPYADQSKVIRISLSKALGDKAYENDNEMYLFRSSVAYANROYELKVKNQ 660
Qy 662 MILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDNS 721
Db 661 MILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDNS 720
Qy 722 LEFTGIQPTLGPNNQPPVSIWLVGVVGMVIVGIVILITGIRDRKKKAKSGENPY 781
Db 721 LEFTGIQPTLGPNNQPPVSIWLVGVVGMVIVGIVILITGIRDRKKKAKSGENPY 780
Qy 782 ASIDISKGENNPGFQNTDDVQTSF 805
Db 781 ASIDISKGENNPGFQNTDDVQTSF 804

RESULT 4
Q8RO10 PRELIMINARY; PRT; 805 AA.
ID Q8RO10
AC Q8RO10
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE RIKEN GDNA 2010305L05 gene.
GN ACE2 OR 2010305L05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026801; AAH26801.1; -.
DR MGD; MGI:1517258; Ace2.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR006025; Zn_Mtpeptdse.
DR Pfam; PF01401; Peptidase M2; 1.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00478; WD_REPEATS; 1.
DR PROSITE; PS00442; ZINC_PROTEASE; 1.
SQ SEQUENCE 805 AA; 92367 MW; D8B883AAC966A8D9 CRC64;
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Query Match 83.4%; Score 3579; DB 11; Length 805;  
Best Local Similarity 82.1%; Pred. No. 6.6e-256;  
Matches 661; Conservative 60; Mismatches 84; Indels 0; Gaps 0;

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Qy 1 MSSSWLLLSLVAVTAQAQSTIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQ 60
Db 1 MSSSWLLLSLVAVTAQAQSTIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQ 60
Qy 61 MNAGDKWSAFLEKQSTLAQMYPLQEIQNLTQVQLQALQALQNGSSVLSDEKSKRLNTIL 120
Db 61 MNAGDKWSAFLEKQSTLAQMYPLQEIQNLTQVQLQALQALQNGSSVLSDEKSKRLNTIL 120
Qy 121 TMSTIYTGKVCNPDNPQECILLPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
Db 121 TMSTIYTGKVCNPDNPQECILLPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
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01-JUN-2001 (TrEMBLrel. 17, Created)  
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 Anigotensin-converting enzyme-related carboxypeptidase.  
 ACE2.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Yamada Y.,  
 Hida M., Tanigami A., Muroi S.;  
 "Molecular cloning, mRNA expression, and chromosomal localization of  
 mouse Angiotensin-converting Enzyme-Related Carboxypeptidase.";  
 Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 [2]  
 SEQUENCE FROM N.A.  
 Komatsu T., Sugano S., Suzuki Y., Hanaoka K., Yamada Y.;  
 "Molecular cloning of ACE2.";  
 Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 EMBL; AB053182; BAB40432.1;  
 MGD; MGI:1917258; Ace2.  
 InterPro; IPR001548; Peptidase\_M2.  
 InterPro; IPR001680; WD40.  
 Pfam; PF01401; Peptidase\_M2; 1.  
 PRINTS; PR00791; PEPTIDASEA.  
 PROSITE; PS00678; WD\_REPEATS\_1; 1.  
 Carboxypeptidase.  
 KQ  
 Carboxypeptidase.  
 SEQUENCE 353 AA; 40442 MW; D17B71141EEA4F5B CRC64;  
 Query Match 35 98; Score 1539; DB 11; Length 353;  
 Best Local Similarity 81.2%; Pred. No. 1.5e-105;  
 Matches 285; Conservative 22; Mismatches 44; Indels 0; Gaps 0;  
 QY 1 MSSSSWLLLSLVAVTAQAQSTIEQAQTLDFKFNHEADLFYQSSLASWNTNITBENVQ 60  
 DB 1 MSSSSWLLLSLVAVTAQAQSTIEQAQTLDFKFNHEADLFYQSSLASWNTNITBENAQ 60  
 QY 61 MNVAGDKWAFLEQSTLAQMYFLOEIQNTLVKQLQALQOQSSVLSSEKSKRLNTIL 120  
 DB 61 KMSEAAAKWAFSEQSKTAQSFSLQIQTPITIKRQLQALQOQSSVLSSEKSKRLNTIL 120  
 QY 121 NTMTSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180  
 DB 121 NTMTSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180  
 QY 181 EBYVVLKNEMARAHYEDYDGYWGDYEVNGVDGYDSRGQIEDVETHEEIKPLYEHL 240  
 DB 181 EBYVVLKNEMARAHYEDYDGYWGDYEVNGVDGYDSRGQIEDVETHEEIKPLYEHL 240  
 QY 241 HAYVRKLMNAYPSYISPGICLPAHLGDMWGRFNTNLYSLTVPFGQKPNIDVTDMVDQ 300  
 DB 241 HAYVRKLMNAYPSYISPGICLPAHLGDMWGRFNTNLYSLTVPFGQKPNIDVTDMVDQ 300  
 QY 301 AWDQRIKFAEKFFSVGLNPMWQGFWNSMLTDPGNVQKAVCHPTAWDL 351  
 DB 301 GWDARIFQEAKEFFSVGLNPMWQGFWNSMLTDPGNVQKAVCHPTAWDL 351  
 RESULT 7  
 Q8N710 PRELIMINARY; PRT; 739 AA.  
 AC Q8N710;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Similar to angiotensin I converting enzyme (Peptidyl-dipeptidase A)  
 DE 1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 Tissue-Testis;  
 Strausberg R.;  
 Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 EMBL; BC036375; AAH36375.1;  
 InterPro; IPR001548; Peptidase\_M2.  
 InterPro; IPR006025; Zn\_Mtpeptidse.  
 Pfam; PF01401; Peptidase\_M2; 1.  
 PRINTS; PR00791; PEPTIDASEA.  
 PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 SEQUENCE 739 AA; 83959 MW; 87995DFE58D93D01 CRC64;  
 Query Match 31.4%; Score 1347.5; DB 4; Length 739;  
 Best Local Similarity 40.4%; Pred. No. 6.7e-91;  
 Matches 266; Conservative 125; Mismatches 224; Indels 43; Gaps 12;  
 QY 16 AAQS---TIBEOAKTFLDKFNHEADLFYQSSLASWNTNITEE-----NVQNMN 63  
 DB 62 SAQSPNLTDEAEAKFVEEDRTSQVWNEYAEANWNTNITETSKILLQKNMQIAN 121  
 QY 64 NAGDKWAFLEQSTLAQMYFLOEIQNTLVKQLQALQOQSSVLSSEKSKRLNTILTM 123  
 DB 122 HT-----LKYGTQARKFDVNQONTTKRIIKVQDLERAALPAQELEYNKLIDM 173  
 QY 124 STIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEY 183  
 DB 174 ETTYSVATVCHPNG--SCLEPDLTNWATSRKYEDLLWAGWGRDKAGRAILOFYPKY 231  
 QY 184 VVLKNEMARAHYEDYDGYWGDYEVNGVDGYDSRGQIEDVETHEEIKPLYEHLHAY 243  
 DB 232 VELINQAARLNGYVDAGSWRSMYETPSLE-----QDLERLFOELQPLYNLHAY 281  
 QY 244 VRKLMNAY-PSYISPGICLPAHLGDMWGRFNTNLYSLTVPFGQKPNIDVTDMVDQ 302  
 DB 282 VRALHRYGACHINLEGPPIPAHLGDMWGRFNTNLYSLTVPFGQKPNIDVTDMVDQ 341  
 QY 303 DAQRIFKEAEKFFSVGLNPMWQGFWNSMLTDPGNVQKAVCHPTAWDLGKG-DPRILMC 361  
 DB 342 TPRRMKEADFFTSGLLPPVPEFWKSMLEKPTDGRVTVCHASAWDFYNGKDFRIKQC 401  
 QY 362 TKVTWDDFLTAHENGHIQYDMAYAAQFLLRNGNEGFHEAVGEINSLSATPKHLKSI 421  
 DB 402 TTVNLEDLVVAHENGHIQYFMQYKDLPLVALREGANPGFHEAIGDVLALSSTPKHLHSL 461  
 QY 422 GLISPDFQEDNTEINFLKQALITVGLTPFTYMLEKRWVMVFKGEIPKQDMKKWEMK 481  
 DB 462 NLLSSEGGSD-EHDINFLMKVADKIAFIPFSYLVQWWRVFDGSIKENTVQEWWSLR 520  
 QY 482 REIVGVPEVPDHEITYCDPASLFHVSNDYSIRYVTRLYQFOQFQALCOAKHEGPHLK 541  
 DB 521 LKYQGLCPVPPTQDGFPGAKFHIPSSVPYIRYFVSPFIQFQFHEALCOAGHTGPHLK 580  
 QY 542 CDISNSTAGOKLFNMLRLGKSEPTLALENVVGAKNMVRPLNLYFFPFLFTWLDQNK- 600  
 DB 581 CDLYQSKAGORLATAMKLGSRPWPPEAMQLITGPNWSASAMLSYFKPLDLWLTENEL 640  
 QY 601 -NSFVGM-STDWSPYAD---QSIKVRISLKGALGKAYEWNDNEMYLFPSSVAYAMRQ 653  
 DB 641 HGEKLGWPOYNWTPNSDDFYNETETKIFLQ--FYDQTGIWDHGAHLLPPLPPQARGTRE 696  
 RESULT 8  
 Q9GLN6 PRELIMINARY; PRT; 732 AA.  
 ID Q9GLN6;  
 AC Q9GLN6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Dipeptidyl carboxy peptidase 1 testicular form.  
 DE DCPI.

OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20469400; PubMed=11013071;  
 RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,  
 RA "Human-Chimpanzee DNA sequence variation in the four major genes of  
 RT the renin angiotensin system";  
 RL Genomics 69:14-26(2000).  
 DR EMBL; AF193476; AAG31359.1; JOINED.  
 DR EMBL; AF193477; AAG31359.1; JOINED.  
 DR EMBL; AF193478; AAG31359.1; JOINED.  
 DR EMBL; AF193479; AAG31359.1; JOINED.  
 DR EMBL; AF193480; AAG31359.1; JOINED.  
 DR EMBL; AF193481; AAG31359.1; JOINED.  
 DR EMBL; AF193482; AAG31359.1; JOINED.  
 DR EMBL; AF193483; AAG31359.1; JOINED.  
 DR EMBL; AF193484; AAG31359.1; JOINED.  
 DR EMBL; AF193485; AAG31359.1; JOINED.  
 DR InterPro; IPR001548; Peptidase M2.  
 DR Pfam; PF01401; Peptidase M2; 1.  
 DR PRINTS; PR00791; PEPDIPITASEA.  
 DR ProDom; PD004184; Peptidase M2; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 DR SEQUENCE 732 AA; 83428 MW; C43D06443A7E74B CRC64;  
 20  
 Query Match 31.1%; Score 1336; DB 6; Length 732;  
 Best Local Similarity 41.6%; Pred. No. 4.7e-90;  
 Matches 256; Conservative 119; Mismatches 205; Indels 38; Gaps 10;  
 QY 15 TAAQ-----TIEQAKTFLDKFNHEADLFYOSSLASWNYNTNITE-----NVQNM 62  
 DB 61 TSAQSNLTDEAAKSFVEEDRTSQVWVEAYEANNYNNTNITETSKILLQNMQIA 120  
 QY 63 NNAGDKWSAFLKEQSLAQWYPIORIONLTVKLQALQONGSSVLSDEKSKRLNTI 122  
 DB 121 NHT-----UKYQARFDFVNDQNTTIKRIKVKQDLERAAALPAQEEYNNKILLD 172  
 QY 123 MSTYTGKVCNPDNPQECILLEPGLNEIMANSLDYNERLWAWESWRSEVKGKLPYEE 182  
 DB 173 METTYSVATVCHTG--SCLQLEPDLTNWATSRKYEDLLWAWEGWDRKAGRAILQFYPK 230  
 QY 183 YVVLKNEMARANYEDYDWRGDIYVNGVDYVSRGQIIEVHTFEEIKPLYLHA 242  
 DB 231 YVELINQARLNGYVDAGDSWRSMTETPSLE-----QDLERLFOELQPLYLNLHA 280  
 QY 243 YVRALKNMAY--PSYISPIGCLPAHLIGDMWGFNTNLSLTVPFGQKPNIDVTDAVDQA 301  
 DB 281 YVRALHRYGACHINLEGPPIAHLGNMAQWTSNIYDLVVPFSPASMD\*TEAMLKQG 340  
 QY 302 WDQRIKFAKEKFFSVGVLPMWTQGWENSMITDPGNOKAVCHPTAWDLGK--DPRILM 360  
 DB 341 WTPRRMFKEADDFTSGLGLVPVPFENKSMLEKPTDGRVWVCHASANDFYNGKDFRIKQ 400  
 QY 361 CTKVTVDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHAEGEIMSLAATPKHLKS 420  
 DB 401 CTTVNLEDLVAAHHEMGHIQYFMOYKDLPAVALREGANPGFHEAIGDVLALSYSTPKLHS 460  
 QY 421 IGLLSDFQEDNETENFLKQALTVGLTPFTYMLEKRWVVFKEIIPKQWMMKWEW 480  
 DB 461 LNLSSGEGSD--EHDNLFMKALDKIAFTIPFSYLVDMWRVDFDGSITKENYNQEWNSL 519  
 QY 481 KREIVGVVEVPDHEITYCDPASLFHVSNDYSFRTYRTLYOFQFOALCQAAKHEGPLH 540  
 DB 520 RLKQGLCPVPPTQGFDFDCAKEFHIPSSVPIRYFVFSITIQFQHEALCQAAGHTGPLH 579

QY 541 KCDISNSTEAGOKLFNMLRLKSEPWTLALENVGAKMVRPLNLYEPELFTWLKDONK 600  
 DB 580 KCDIYQSKEAGORLATAMKGLFSREWPBAMQLITQPNNSASAMLSYFKPLDMLWTENE 639  
 QY 601 --NSFWG--STDWSPYADQS 617  
 DB 640 LHGEKLGWPPQYNTWTPNSARS 659  
 RESULT 9  
 Q8K233 PRELIMINARY; PRT; 1015 AA.  
 ID Q8K233  
 AC Q8K233  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ACE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034367; AAH34367.1; -.  
 DR MGD; MGI:87874; Ace.  
 DR InterPro; IPR001548; Peptidase M2.  
 DR InterPro; IPR006025; Zn\_MTPeptase.  
 DR Pfam; PF01401; Peptidase M2; 2.  
 DR PRINTS; PR00791; PEPDIPITASEA.  
 DR ProDom; PD004184; Peptidase M2; 2.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 2.  
 KW Hypothetical protein.  
 FT NON TER  
 SQ SEQUENCE 1015 AA; 117509 MW; D097F69585553C27 CRC64;  
 Query Match 31.1%; Score 1334; DB 11; Length 1015;  
 Best Local Similarity 42.6%; Pred. No. 1.1e-89;  
 Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;  
 QY 20 TIEQAKTFLDKFNHEADLFYOSSLASWNYNTNITEVQNNNAGDKWSAFLKEQSL 79  
 DB 415 TDAKADRFVEEDRTAQVLLNEAYEANNYNNTIIEGSKILLEKSTEVNHTLVGTR 474  
 QY 80 AQMYPLQEIQNLTKVQLQALQONGSSVLSDEKSKRLNTIINTMTIYSTGKVCNPDNPQ 139  
 DB 475 AKTFDVSNFQNSIKRIKKLQNLDRAVLPPEKEEYNQILLDMETYSLSNICYTNG-- 532  
 QY 140 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVKGKLPYEEYVVLKNEMARANYEDY 199  
 DB 533 TCMPLPDLTNWATSRKYEELLWAWESWRDKVGRAILPFPKYVFSNKIAXLNGYTD 592  
 QY 200 GDYWRGDIYVNGVDYVSRGQIIEVHTFEEIKPLYLHAAYRAKLMNAYPS-YISP 258  
 DB 593 GDSNRSLYESDNLE-----QDLKLYQLQLPLYLNLHAYVRSRLHRRHGYSEYINL 642  
 QY 259 IGCLPAHLIGDMWGFNTNLSLTVPFGQKPNIDVTDAVDQAQRIKFAKEKFFSV 318  
 DB 643 DGPIPAHLGNMAQWTSNIYDLVAPFSPAPNIDATEAMIKQGTWTRIFKEADNFTSL 702  
 QY 319 GLPNMTQGFWENSMITDPGNOKAVCHPTAWDLGK--DPRILMCTKVTVDDFLTAHHEMG 377  
 DB 703 GLLPVPPEFVWKNMSEKPTDGRVWVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMG 762  
 QY 378 HIQYDMAYAAQPFLLRNGANEGFHAEGEIMSLAATPKHLKSIGLLSPDFQEDNETEIN 437  
 DB 763 HIQYFMOYKDLPTVTFREGANPGFHEAIGDMLASVSTPKELYSINLST--GSGYEYDIN 821  
 QY 438 FLLKQALTVGLTPFTYMLEKRWVVFKEIIPKQWMMKWEKREIVGVVEVPDHEITY 497







SQ SEQUENCE 619 AA; 69377 MW; 4FF26269AF79596AD CRC64;  
 Query Match 25.6%; Score 1100.5; DB 16; Length 619;  
 Best Local Similarity 37.8%; Pred. No. 9.6e-73;  
 Matches 235; Conservative 101; Mismatches 246; Indels 39; Gaps 13;  
 QY 7 LLSLVAVTAAQSTIE-----EQAKTFLDKFNHEAEDLFQSSLSAWNYNT 52  
 Db 17 LTLNLTACNNKQNTSEYKTSIPASTSTPDKAQAIAFIQDAEAQMAQLSTEANRAEWISN 76  
 QY 53 NTEENVQNMNAGDKWSAFLEKQSTLAQMYPLOEIQNTLV-KLQALAQNGSSVLSED 111  
 Db 77 FITEDTAALSAAVGEKYSAAVSFKATEAAKYANVELDPANARKIMILRSALVLPAPLDP 136  
 QY 112 KSKRLNTILNTWSTIYTGKVCNPNQPOECLLEPEGLNEIMANSIDYNERLMAWESWSE 171  
 Db 137 KNAELAQAQSSSELNGLYGKGYCPADG--KC-MTQPELSSILMAESRDPAKLLEAWKGR-E 192  
 QY 172 VQKQLRPILYEYVVLKHEMARAHYEDYGYWRGDEVNGVDGYDYSRGQLIEDVEHTFE 233  
 Db 193 IAKPRPILPQREVELANEGAKDLGYANLSLWRSQ-----YDMKPDSPSQELDLRLWS 244  
 QY 232 EIKPLYEHLHYAVRAKLMNAYPSYISP-IGCLPAHLLEGDMWGRFWTNLYSLTFVPFGQKPN 290  
 Db 245 QVKPLYESLHCYVRGELNKEYGDALAPKTGPFAHLHGNWMAQQMGVYDLVAPENADPG 304  
 QY 291 IYVTDAMVDQAWDAQRFKCAEKFVSGLPWNTOGFWNSMLTDPGNVOKAVCHPTAWD 350  
 Db 305 YDVTLLAQKGYDHRVMYQAESFFTSLSGPAFLPDSFWRSLSFLQPKD-RDVVCHASAWD 363  
 QY 351 LQK-GDPRILMCTKVYTMDDFLTAHHEMGHTQYDMAYAAQPFLLRNGANEHGEAVGEIMS 409  
 Db 364 LQNLDDIRIKWCIOKTAEDFVTHHELGHNFYQRAYKQFPFLFKNSANDGPFHEAIGDTIA 423  
 QY 410 LSAATPKHLKSGILIS--PPQEDNETEINFLKQALTIVGLPFTYMLKXRMVFKGE 467  
 Db 424 LS-ITPSYLKQIGLLEEVDPASKD---IGLLLKQALDKIAFLPFLGLMIDQWRWKFVSGE 478  
 QY 468 IPKDQMKKKWEMKREIVGVVPEVPHDDETYCDPASLFHVSNDYSFTRYTYRTRYLQFOQEE 527  
 Db 479 ITPAQYNQAWELREKYGKVKAPPTFSETDFDGAKYHVPGNVPTRYFLAHLQFOFKH 538  
 QY 528 ALCOAAKEGHLHKCDTNSSTEAGKLFNMLRLKSEPTTLAENVVGAKMNVREPLNLY 587  
 Db 539 ALCEATAGDKGVHRCISYGNQAAGEKLNRMLEIGSSQPPMALKEVTGTETMDANAVLDY 598  
 QY 588 REPLEFTLWKDQNK--NSFVGV 606  
 Db 599 FAPLKTWLDEQNKAANRCCGW 619  
 RESULT 15  
 Q9NDS8 PRELIMINARY; PRT; 648 AA.  
 ID Q9NDS8 AC Q9NDS8;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ecodysteroid-inducible angiotensin-converting enzyme-related gene  
 DE product.  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 RN NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CI08; TISSUE=Wing imaginal disk;  
 RX MEDLINE=2056050; PubMed=1102839;  
 RA Quan G.X., Mica K., Okano K., Shimada T., Ugajin N., Xia Z., Goto N.,  
 RA Kanke E., Kawasaki H.;  
 RT "Isolation and expression of the ecodysteroid-inducible angiotensin-  
 RT converting enzyme-related gene in wing discs of Bombyx mori."

```
RL Insect Biochem. Mol. Biol. 31:97-103 (2001).
DR EMBL: AB026110; BAA97657.1; -.
DR MERO89: M02.002; -.
DR InterPro: IPR001548; Peptidase_M2.
DR InterPro: IPR006025; Zn_MTPeptidase.
DR Pfam: PF01401; Peptidase_M2; 1.
DR PRINTS: PR00791; PEPTIDTASEA.
DR ProDom: PD004184; Peptidase_M2; 1.
DR ProSITE: PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 648 AA; 74917 MW; 9A740AA9FCACEBF0 CRC64;

Query Match 25.48; Score 1089.5; DB 5; Length 648;
Best Local Similarity 35.67; Pred. No. 6.7e-72; Indels 35; Gaps 11;
Matches 232; Conservative 125; Mismatches 259;

QY 11 LVAVTAQSTIEQAK-TFLDKFNHEADLFY-----QSSLASWNYNTNTEEN 58
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 10 LIAAIVAVFIVATQGRPDLEAREHREAYMLHLDKATGLRKNRASLAWEYTSNITKEN 69
QY 59 VQNNNAGDKWSAFLKEQSTLAQMYPLQETQNLTKLQALQONGSSVLSDEKSKLNT 118
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 EEKSIQTHLELSRQEKAAEETKMYGQDFDFTLRMFKKYSQLGVAALPDDKFGALMR 129
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 ILNTWSTIYTGKVCNPDNPOEC-LLLEPGILNEIMANSLDYNBELWAWESWRSEVGKQLR 177
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 TVSGMESNYATKICSYKNESKCDLSLEPEITEIFSTQDPPEELKHAWEWHNAAGATAK 189
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 178 PLIEEYVVLKEMARAHYEDYGRGDYVNGDGYDSRGOLIEDVEHTEETKPLY 237
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 KNFTDYVNLNEAAKNGFDNVAEWQSEYEVDPFE-----EQAKLMEDVAKPLY 239
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 238 EHLHAYVRAKLNNAY-PSYISPIGCLPAHLGLDMGRFWTNLYSLTVPFGQKPNIDVTD 296
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 240 QQLHAYVVKRLRDYKGVKVSARGPIPAHLGLGNWQAQTWNIESFTRPYDPKKEIDVTA 299
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 297 MVDQAWDAQRIFKEAEKFFVUGLNNMTQGTWNSMLTDPGNVOKAYCHPTAMDLGK-D 355
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 MRDQNYTPMKMFQMSDEFPSNLNTAMPEKFWKNSIIIEKPTD-REIVCHASANDFFDGED 358
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 356 PRILMCTKVTDDELTAHEHMGHIOYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATP 415
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 359 FRIKQCTTVDYVEYFQTHHEMGHIOYLYQYRDQPVVFDGANGQGFHEAVGDTIALSVSSP 418
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 416 KHLKSGILSLSPQBDNTEINFLKQALITVGTLPFTYMLEKWRWVFKGEIPEQDQWK 475
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 419 KHLRVGLATGD-AEDEQTEINQLYKMGIDKIAFLFFAYTLDLFRYGVFREKTLPEIDYNC 477
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 476 KWEKREIVGYVEVPVPHDETYCDPASLFHYSNDYSFIRYVTRTYQFQFOEALCO-AAK 534
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 478 HYWKUREQQGVPEPPNRTEDDFDAAKYHVSNNVEYARYVVSFIQFPHRGVCQLAGE 537
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 535 HEG-----PLHKCDISNSTEAGOKLFNMLRLGKSEFWTLALENVVGAKNMVRPLLNYFE 589
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 538 HAAGDPNKKLVDCDIYQSVAAGNALANMLKMGSSKFPDAMEALTQREMKAADGLLEYFR 597
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 590 PLFTWLDQNKNS--FVGHSTDSVPYADQSIKVRISLKSALGDKAYEWNNDN 638
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 598 PLHDWLRAENQRTGHEHIGWPTNMEYCTPSQLSELNVKEPSSSPATQOSDS 648
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: February 19, 2004, 19:51:08  
Job time : 45 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2004, 19:47:53 ; Search time 21 Seconds  
(without alignments)  
3686.466 Million cell updates/sec

Title: US-09-163-648-2

Perfect score: 4291

Sequence: 1 MSSSSMLLSLVATAAQT.....ISKGNNPGFQNTDDVQTGF 805

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76:\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	4281	99.8	804	2	T14762
2	1344	31.3	732	1	S05238
3	1337	31.2	1306	1	A31759
4	1334	31.1	732	1	A35655
5	1334	31.1	1312	1	A34171
6	1312	30.6	1193	2	JC2489
7	1310	30.5	1313	1	JC2038
8	1283	29.9	737	1	A34402
9	1283	29.9	1309	1	S35484
10	1058	24.7	611	2	S65472
11	1039	24.2	615	2	A57533
12	1030	24.0	630	2	JS5374
13	642.5	15.0	907	2	T15792
14	157	3.7	532	2	C83696
15	154	3.6	502	2	AF1310
16	147	3.4	502	2	A21682
17	139.5	3.3	987	2	A12011
18	139	3.2	608	2	B82938
19	136	3.2	611	2	D82881
20	135	3.1	501	2	D59943
21	125	2.9	627	1	S40048
22	124.5	2.9	987	2	I48373
23	124	2.9	538	2	E92561
24	123.5	2.9	902	2	E90270
25	123	2.9	990	2	S23416
26	122	2.8	642	2	B98000
27	121	2.8	607	2	AB3511
28	121	2.8	1034	2	T30574
29	120	2.8	1339	2	A84683

30 119.5 2.8 1283 2 S52500  
31 119.5 2.8 3655 2 T38084  
32 119.5 2.8 4540 2 T30838  
33 118.5 2.8 1780 2 T17272  
34 118 2.7 642 2 G95129  
35 117 2.7 1575 2 G82905  
36 116 2.7 963 2 C90535  
37 116 2.7 1642 2 T08880  
38 116 2.7 1939 2 D97316  
39 115.5 2.7 611 2 A75573  
40 115.5 2.7 3433 1 S28381  
41 115 2.7 524 2 B82202  
42 115 2.7 950 2 A71655  
43 115 2.7 952 2 T50451  
44 114.5 2.7 901 2 A48653  
45 114.5 2.7 1225 1 B64234

ALIGNMENTS

RESULT 1

T14762  
hypothetical protein DKFP434A014.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T14762  
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, August 1999  
A:Reference number: Z18181  
A:Accession: T14762  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-804 <WAM>  
A:Cross-references: EMBL:AL110224  
A:Experimental source: adult testis; clone DKFP434A014  
C:Genetics:  
A:Note: DKFP434A014.1

Query Match 99.8%; Score 4281; DB 2; Length 804;  
Best Local Similarity 99.9%; Pred. No. 6.9e-288;  
Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2	SSSSMLLSLVATAAQTIEQAKTFLDKFNHEADLFYQSSLASWYNNTNTEENVON	61
DB	1	SSSSMLLSLVATAAHTSTIEQAKTFLDKFNHEADLFYQSSLASWYNNTNTEENVON	60
QY	62	MNAGDKWSAFLEKEOSTLAQMYPLQBIQNLTVKLOLQALQONGSSVLSSEKSKRLNTILN	121
DB	61	MNAGDKWSAFLEKEOSTLAQMYPLQBIQNLTVKLOLQALQONGSSVLSSEKSKRLNTILN	120
QY	122	TWSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESWSEVKQRLPIYE	181
DB	121	TWSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESWSEVKQRLPIYE	180
QY	182	EYVLKNEWARANHYEDYDGYRGGYEVNGVDGYDSRGQLIEDVEHTFEETKPLYEHLH	241
DB	181	EYVLKNEWARANHYEDYDGYRGGYEVNGVDGYDSRGQLIEDVEHTFEETKPLYEHLH	240
QY	242	AYVRKIMNAPSYISPIGCLPAHLIGDMWGFNWTNLYSLTVPPFGQKNIDVTDAMVQA	301
DB	241	AYVRKIMNAPSYISPIGCLPAHLIGDMWGFNWTNLYSLTVPPFGQKNIDVTDAMVQA	300
QY	302	WDAQRIKFAEKFFVSGVLPNNMTQGFWNSMLTDPNQKAVCHPTAMDGLGKDFRILMC	361
DB	301	WDAQRIKFAEKFFVSGVLPNNMTQGFWNSMLTDPNQKAVCHPTAMDGLGKDFRILMC	360
QY	362	TKVTMDDFLTAFHEMGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKSI	421
DB	361	TKVTMDDFLTAFHEMGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKSI	420
QY	422	GLISPPQEDNETEINFILKQALTIVGTLPFTVLEKWEVYFKGEIPKQDQWKKWENK	481

Db 421 GLLSPDFQEDNETENFLKQALITVGLTPTTYMLEKWRWVFKGEITPKDQWKKWEMK 480  
QY 482 RIIVGVVPEVPHDETYCDPASLFHVSNDYSPRIYVTRLYQFOFOEALCOAKHGGPLHK 541  
Db 481 RIIVGVVPEVPHDETYCDPASLFHVSNDYSPRIYVTRLYQFOFOEALCOAKHGGPLHK 540  
QY 542 CDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKNNVRLPLNYPPEPLFTWLKQDNKN 601  
Db 541 CDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKNNVRLPLNYPPEPLFTWLKQDNKN 600  
QY 602 SFVGSWTDSPVADOSIKVRISLKSALGDKAYEWDNEMYLFRSSVAYAMEQYFLVKVQK 661  
Db 601 SFVGSWTDSPVADOSIKVRISLKSALGDKAYEWDNEMYLFRSSVAYAMEQYFLVKVQK 660  
QY 662 MILFGEEDVRANLKRPRISNFVFTAPKNVSDIIIPRTEVEKAIRMSRRIINDAFRLDNS 721  
Db 661 MILFGEEDVRANLKRPRISNFVFTAPKNVSDIIIPRTEVEKAIRMSRRIINDAFRLDNS 720  
QY 722 LBLFLGIQPTLGPNNQPPVSIWLVFGVVGVIWVGIVILIFGTIRDRKKKNKARSGENPY 781  
Db 721 LBLFLGIQPTLGPNNQPPVSIWLVFGVVGVIWVGIVILIFGTIRDRKKKNKARSGENPY 780  
QY 782 ASIDISKGNNGFQNTDDVQTSF 805  
Db 781 ASIDISKGNNGFQNTDDVQTSF 804

RESULT 2  
S05238  
peptidyl-di-peptidase A (EC 3.4.15.1) precursor, testicular splice form - human  
N:Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypeptidase  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1991 #sequence\_revision 02-Jul-1998 #text\_change 18-Jun-1999  
C:Accession: S05238; A33979  
R:Lattion, A.L.; Soubrier, F.; Allegrini, J.; Hubert, C.; Corvol, P.; Alhenc-Gelas, F.  
FEBS Lett. 252, 99-104, 1989  
A:Title: The testicular transcript of the angiotensin I-converting enzyme encodes for the  
A:Reference number: S05238; MUID:89338720; PMID:2547653  
A:Accession: S05238  
A:Molecule type: mRNA  
A:Residues: 1-732 <EHL>  
A:Cross-references: EMBL:X16295; NID:g28264; PIDN:CAA34362.1; PID:g28265  
R:Enlars, M.R.W.; Fox, E.A.; Stridom, D.J.; Riordan, J.F.  
Proc. Natl. Acad. Sci. U.S.A. 86, 7741-7745, 1989  
A:Title: Molecular cloning of human testicular angiotensin-converting enzyme: the testis  
A:Reference number: A33979; MUID:90046671; PMID:2554286  
A:Accession: A33979  
A:Molecule type: mRNA  
A:Residues: 1-732 <EHL>  
A:Cross-references: GB:M26657; NID:g338666; PIDN:AAA60611.1; PID:g338667  
A:Experimental source: clones R1.2 and T8B  
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown  
C:Comment: For the renal and pulmonary splice form, see PIR:A31759.  
C:Genetics:  
A:Gene: GDB:DCP1; ACE  
A:Cross-references: GDB:119840; OMIM:106180  
A:Map position: 17q23-17q23  
C:Function:  
A:Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptide  
C:Superfamily: mammalian peptidyl-di-peptidase A  
C:Keywords: alternative splicing; glycoprotein; metalloproteinase; peptidyl dipeptide hydrolase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-732/Product: peptidyl dipeptidase I #status predicted <MAT>  
F:686-702/Domain: transmembrane #status predicted <TRM>  
F:103,121,140,186,368,617,651/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:414,418,434/Binding site: zinc, catalytic (His, His, Glu) #status predicted  
F:415/Active site: Glu #status predicted

Query Match 31.3%; Score 1344; DB 1; Length 732;  
Best Local Similarity 41.8%; Pred. No. 7.7e-85;  
Matches 259; Conservative 119; Mismatches 204; Indels 38; Gaps 10;

QY 15 TAAQS-----TIEQAKTFLDKFNHEADLFYQSSLASWNTNITEE-----NVQNM 62

Db 61 TSAQSNLVTDEAEASKFVEEYDRTSQVVMNAYAEANMNTNITETSKILLQKMQIA 120  
QY 63 NNAAGKWSAFLKEQSTLAQWYPLQEIQLNTLVKLQALQONGSSVLSLDSKRLNTILNT 122  
Db 121 NHT-----LKYGTQARKFDVNLQNTTIKRIKKVQDLERAAALPAQELBEYNKILLD 172  
QY 123 MSTIYGTGVCVNDPNDPQECILLLEPGLINEIMANSLYNERLWAWESRSEVGGQAPLYEE 182  
Db 173 METTYSVATVCHPNG--SCLQLEPDLTNYMATSRKYEDLLAWEGWRDQAGRAILQFYFYPK 230  
QY 183 YVVLKMEMARAHYEDYGYWGRGVGVGDYVSRGQLIEDVEHTFEIIPKLYEHLHA 242  
Db 231 YVLEINQAARLNGYVDAGSWRSWYETPSLE-----QDLERLPQELQPLYLNLHA 280  
QY 243 YVRAKLWAY-PSYISPIGCLPAHLIGDMGWFNTNLYSLTVPFGQKPNIDVTDAMVQQA 301  
Db 281 YVRAALRHRYGAHINLEGPFAHLILGNMWAQTNISYDLVVVFPFAPSMDTTEAMLKQG 340  
QY 302 WDAQRIFKAEKFFSVGLPNMTQGFWENSMITDPGNVQKAVCHPTAWDLGKG-DPRILM 360  
Db 341 WTPRRMFKAEADFFSLGLLPVPEPFWNKSMLEKPTDGREVVCHASANDFYNGKDFRIKQ 400  
QY 361 CTKVYMDDFLTAHHEMGIHQYDMAYAAQPFLLRNGANEGFHEAVGIMSLSAATPKLKS 420  
Db 401 CTTVNLDELVAHHEMGIHQYFMQYKDLFPVALREGANPGFHEAIGDVLALSVPKHLHS 460  
QY 421 IGLSPDFQEDNETENFLKQALITVGLTPTTYMLEKWRWVFKGEITPKDQWKKWEMK 480  
Db 461 INLLSSGGSD-EHDLNLFMKALDKIATIPFSYLVVDQWRVFDGSIITKENYNQEWWSL 519  
QY 481 KREIVGVVPEVPHDETYCDPASLFHVSNDYSPRIYVTRLYQFOFOEALCOAKHGGPLH 540  
Db 520 RLKYQGLCPVPRTQGDFFDGAKEFHIPSSVPYIRYFVSFIQFQFHEALCOAAHGTPHLH 579  
QY 541 KCDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKNNVRLPLNYPPEPLFTWLKQDNKN 600  
Db 580 KCDIYQSKQAGQRLATAMKLGFRSPFPAEMQLITGQPNWSASAMLSYFEPKLLDLRLTENE 639  
QY 601 --NSFVGW-STDWSPYADQS 617  
Db 640 LHGEKLGWPQYNTFNSARS 659

RESULT 3  
A31759  
peptidyl-di-peptidase A (EC 3.4.15.1) precursor, renal and pulmonary splice form - human  
N:Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypeptidase  
C:Species: Homo sapiens (man)  
C:Date: 07-Jun-1990 #sequence\_revision 02-Jul-1998 #text\_change 18-Jun-1999  
C:Accession: A31759; PQ0004  
R:Soubrier, F.; Alhenc-Gelas, F.; Hubert, C.; Allegrini, J.; John, M.; Tregear, G.; Co  
Proc. Natl. Acad. Sci. U.S.A. 85, 9386-9390, 1988  
A:Title: Two putative active centers in human angiotensin I-converting enzyme revealed  
A:Reference number: A31759; MUID:89071703; PMID:2849100  
A:Accession: A31759  
A:Molecule type: mRNA  
A:Residues: 1-1306 <SOU>  
A:Cross-references: GB:J04144; NID:g178285; PIDN:AAA51684.1; PID:g178286  
A:Experimental source: kidney  
A:Note: parts of this sequence, including the amino end of the mature protein, were derived from a cDNA clone of the human angiotensin I-converting enzyme, H. Takeuchi, K.; Shimizu, T.; Ohishi, N.; Seyama, Y.; Takaku, F.; Yotsumoto, H.  
J. Biochem. 106, 442-445, 1989  
A:Title: Purification of human lung angiotensin-converting enzyme by high-performance  
A:Reference number: PQ0004; MUID:90110025; PMID:2558109  
A:Accession: PQ0004  
A:Molecule type: protein  
A:Residues: 'XX', 32-34, 'E', 36-37, 'X', 39-41, 'R', 43-46 <TAK>  
A:Experimental source: lung  
C:Comment: This splice form is found in many tissues, in particular kidney and lung  
C:Genetics:  
A:Gene: GDB:DCP1; ACE  
A:Cross-references: GDB:119840; OMIM:106180

A:Map position: 17q23-17q23

A:Function:  
C:Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptide  
A:Note: plays a role in the control of blood pressure by catalyzing the conversion of an  
C:Superfamily: mammalian peptidyl-dipeptidase A  
C:Keywords: alternative splicing; blood pressure control; glycoprotein; kidney; lung; me  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-1306/Product: peptidyl dipeptidase I #status predicted <MAT>  
F:1260-1276/Domain: transmembrane #status predicted <TRM>  
F:38,54,74,111,146,160,318,445,509,523,677,695,714,760,942,1191,1225/Binding site: carbo  
F:330,394/Binding site: zinc (His) #status predicted  
F:988,992,1008/Binding site: zinc, catalytic (His, His, Glu) #status predicted  
F:989/Active site: Glu #status predicted

Query Match 31.2%; Score 1337; DB 1; Length 1306;  
Best Local Similarity 41.7%; Pred. No. 5.7e-84;  
Matches 255; Conservative 118; Mismatches 204; Indels 34; Gaps 9;  
QY 20 TIEQAKTFLDKFNHEADLFYQSSLASWYNTNITE-----NVQNMNAGDKWSA 71  
DB 644 TDEAEASKFVEYDRTSQVWNEAYEANWYNTNITTETSKILLQKMQIANHT----- 697  
QY 72 FLXQSTLAQMPYQETQNLVKLOALQONGSSVLSDEKSKRLNTILNTMTSTIYSTGK 131  
DB 698 --LXGTCARFQVNLQNTIKI IKVQDLERAPLPAQELBEYNNKILLDMETTSVAT 755  
QY 132 VCNPDNPOECLLLPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMA 191  
DB 756 VCHPNG--SCLQLEPDLTNVMTATSKYEDLLWAEGRDQAGRAILOFYPKYVELINQAA 813  
QY 192 RANHYEDGYVRGDYEVNGVDGYDSRGQLIEDVHTFBEIKPLYEHLHAYVRAKLMNA 251  
DB 814 RLNGYVADGDSWRSMYETPSLE-----QDLERLFOELQPLYLNLHAYVRRALHRH 863  
QY 252 Y-PSYISPIGCLPAHLGDMGRFWNLVSLTVFGKPNIDVTDAMVQAWDAQRIKFE 310  
DB 864 YGACHINLEGPIPAHLGDMGRFWNLVSLTVFGKPNIDVTDAMVQAWDAQRIKFE 923  
QY 311 AKKPFVSVGLPMTQGFWENSLTDGPNVQKAVCHPTAMD LGK--DFRILMCTKVTTMDDF 369  
DB 924 ADDFTTSUGLLPVPPEFNNKSMLEKPTDGRVVCCHASANDFYNGKDFRIKQCTVNL 983  
QY 370 LTAHEMGHIQYDWAYAAQFLLRNGANEGFHEAVGEIMSLSAATPKHLKSGILLSPDFQ 429  
DB 984 VVAHEMGHIQYFMQYKDLPLVALREGANFGFHEAIGDVALSVSTPKHLKSLNLSSEG 1043  
QY 430 EDNETEINFLKQALTIQVTLPTMYLKKRWVFKGEIPKQDMKKWEMKREIVGVVE 489  
DB 1044 SD-EHDINFLMKQALDKIAFPFSLVDQWRVDFGSIITKENYQEWWSLRLKYQGLCP 1102  
QY 490 PVPHDQTCDPASLPHVSNDSFYRYRTLYQFQFQALCQAAKHEGPHLKCDISNSTE 549  
DB 1103 PVPRTOGDFDGAKEPHISSPYRYRYFVSFIIOFQFHEALCQAAAGHTGPHLKCDIYQ 1162  
QY 550 AQCKLFLNMLRCKSPWTLALENVVGAKNMVRPLNYPFLPTWLDQNK--NSFVGM- 606  
DB 1163 AQORLATAMKLGFSRWPENAMOLITGQPNMSASAMNIFRPLTEWLVNRRHGEILGWPEY 1222  
QY 607 STDWSPYADQS 617  
DB 1223 QYNWTPNSARS 1233

## RESULT 4

A35655  
peptidyl-dipeptidase A (EC 3.4.15.1), testis - mouse  
N:Alternate names: peptidyl-dipeptidase I, testis  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A35655  
R:Howard, T.E.; Shai, S.Y.; Langford, K.G.; Martin, B.M.; Bernstein, K.E.  
Mol. Cell. Biol. 10, 4294-4302, 1990  
A:Title: Transcription of testicular angiotensin-converting enzyme (ACE) is initiated w/

A:Reference number: A35655; MUID:90318396; PMID:2164636

A:Accession: A35655  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-732 <HOW>  
A:Cross-references: GB:M55333; NID:G191589; PIDN:AAA37149.1; PID:G191590  
A:Superfamily: mammalian peptidyl-dipeptidase A  
C:Keywords: alternative splicing; peptidyl dipeptide hydrolase; transmembrane protein; z

Query Match 31.1%; Score 1334; DB 1; Length 732;  
Best Local Similarity 42.6%; Pred. No. 3.8e-84;  
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

QY 20 TIEQAKTFLDKFNHEADLFYQSSLASWYNTNITE-----NVQNMNAGDKWSAFLKEQSTL 79  
DB 69 TDEAEASKFVEYDRTSQVWNEAYEANWYNTNITEGSKILLEKSTEVSHILKYCTR 128  
QY 80 AQMPYQLQIQNLTKVLQALQONGSSVLSDEKSKRLNTILNTMTSTIYSTGKVCNPDNPQ 139  
DB 129 AKTFDVSFQNSIKRIKKLQNLDRVLPPEKEEYNNQILLDMETTSLSNICVTNG-- 186  
QY 140 ECLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMARANHVEDY 199  
DB 187 TCMLEPDLTNVMTATSKYEDLLWAEGRDQAGRAILOFYPKYVELINQAA 246  
QY 200 GYWRGDYVRGDYEVNGVDGYDSRGQLIEDVHTFBEIKPLYEHLHAYVRAKLMNAYS- YISP 258  
DB 247 GDSWASLVESDNL-----QDLKLYQELQPLYLNLHAYVRRSLHRHYSYINL 296  
QY 259 ICCLPAHLGDMGRFWNLVSLTVFGKPNIDVTDAMVQAWDAQRIKFEAEKFFVSV 318  
DB 297 DGPPIPAHLGDMGRFWNLVSLTVFGKPNIDVTDAMVQAWDAQRIKFEAEKFFVSV 356  
QY 319 GLPNMTQGFWENSLTDGPNVQKAVCHPTAMD LGK--DFRILMCTKVTTMDDFPLTAHEMG 377  
DB 357 GLLPVPPEFNNKSMLEKPTDGRVVCCHASANDFYNGKDFRIKQCTVNL 416  
QY 378 HIQYDWAYAAQFLLRNGANEGFHEAVGEIMSLSAATPKHLKSGILLSPDFQEDNETEIN 437  
DB 417 HIQYFMQYKDLPLVALREGANFGFHEAIGDVALSVSTPKHLKSLNLSSTE--GSGYEYDIN 475  
QY 438 FLKQALTIQVTLPTMYLKKRWVFKGEIPKQDMKKWEMKREIVGVVPPVPHDQTY 497  
DB 476 FLKQALTIQVTLPTMYLKKRWVFKGEIPKQDMKKWEMKREIVGVVPPVPHDQTY 535  
QY 498 CDPASLPHVSNDSFYRYRTLYQFQFQALCQAAKHEGPHLKCDISNSTPAGOKLFNM 557  
DB 536 FDPGSKFHPANVPYRYFVSFIIOFQFHEALCQAAAGHTGPHLKCDIYQSKAGKLLADA 595  
QY 558 LRLGKSEPTLALENVVGAKNMVRPLNYPFLPTWLDQNK--NSFVGM-STDWSP 612  
DB 596 MKLGYSKPPEAKMLITGQPNMSASAMNIFRPLTEWLVNRRHGEILGWPEYKNAP 653

## RESULT 5

A34171  
peptidyl-dipeptidase A (EC 3.4.15.1) precursor - mouse  
N:Alternate names: ACE; angiotensin-converting enzyme; carboxycathepsin; dipeptidyl car  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A34171; A29220; A61477  
R:Bernstein, K.E.; Martin, B.M.; Edwards, A.S.; Bernstein, E.A.  
J. Biol. Chem. 264, 11945-11951, 1989  
A:Title: Mouse angiotensin-converting enzyme is a protein composed of two homologous do  
A:Reference number: A34171; MUID:89308599; PMID:2545691  
A:Accession: A34171  
A:Molecule type: mRNA  
A:Residues: 1-1312 <BER>  
A:Cross-references: GB:J04947  
R:Bernstein, K.E.; Martin, B.M.; Bernstein, E.A.; Linton, J.; Striker, L.; Striker, G.  
J. Biol. Chem. 263, 11021-11024, 1988  
A:Title: The isolation of angiotensin-converting enzyme cDNA.  
A:Reference number: A29220; MUID:88298730; PMID:2841132

A:Accession: A29220  
A:Molecule type: mRNA  
A:Residues: 1-332 <BE2>  
A:Cross-references: GB:J03940; NID:G191593; PIDN:AAA37146.1; PID:G191594  
R:Bernstein, K.E.; Martin, B.M.; Striker, L.; Striker, G.  
Kidney Int. 33, 652-655, 1988  
A:Title: Partial protein sequence of mouse and bovine kidney angiotensin converting enzyme  
A:Reference number: A61477; MUID:88215372; PMID:2835538  
A:Accession: A61477  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 35-54 <BE3>  
A:Experimental source: kidney  
C:Superfamily: mammalian peptidyl-dipeptidase A  
C:Keywords: alternative splicing; blood pressure control; membrane protein; peptidyl-dipeptidase A  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-1312/Product: peptidyl dipeptidase I #status predicted <MAT>

Query Match 31.1%; Score 1334; DB 1; Length 1312;  
Best Local Similarity 42.6%; Pred. No. 9,3e-84;  
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

QY 20 TIERAKFLDFKFNHAEDELFCSSLASWNTNTITEENVQNMNAGDKWAFLEQSTL 79  
DB 649 TDEAKADRFVEYDRTAQVLLNEYAEANQYNTNITIGSKILLEKSTEVSHHTLYGTR 708

QY 80 AQMPLOEIQNLTVKLOLQALQONGSSVLSDEKSKRLNTLNTMTSTYSGKVCNPNQ 139  
DB 709 AKTFDVSNFQNSIKRIKKQLNDRAVLPPKELESEYNQILLDMETTYSLNICYNG-- 766

QY 140 ECLLEPGLNETMANSLDYNERLWAWESRSEVQKQLRPLVEEYVVLKNEVARANHYEDY 199  
DB 767 TCMPEPDLTNNMATSRSKYEEILLMAKWSRDKVGRALILPFPKYVPEPSKTKLNGYTD 826

QY 200 GDYWGDYEVNGVDGYDSRGQLIEDVEHTFEEIKPLYLEHLHAYVRKLMNAYPS-YISP 258  
DB 827 GDSWRSLSYSDNLE-----QDLEKLYQELQPLYLNLHAYVRRSLRHHYSEYINL 876

QY 259 IGLPFAHLGDMWGRFWTNLYSLTVFPQGNKPIDVTDMVDQAWDAQRIKFAEAKFFVS 318  
DB 877 DGIPIPAHLGDMWGRFWTNLYSLTVFPQGNKPIDVTDMVDQAWDAQRIKFAEAKFFVS 936

QY 319 GLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKG-DPRILMCTKVMTDDFLTAHENG 377  
DB 937 GLLPVPEFNNKSMLEKPTDGRVWCHPSAWDFYNGKDFRIKQCTSVNMEDIVIAHENG 996

QY 378 HIQYDMAYAAQPLLRNGANEGHFAVEIGMSLSAATPKHLKSIIGLLSPDQEDNTEI 437  
DB 997 HIQYFMQYKDLPTVTFREGANPGFHEAIGDIMALSVSTPKHLKSIIGLLSPDQEDNTEI 1055

QY 438 FLKQALTIIVGLTLPFTYMLEKRWVFKGEIPKQDMKKWEMKREIVGVVPEVPHDET 497  
DB 1056 FLKQALTIIVGLTLPFTYMLEKRWVFKGEIPKQDMKKWEMKREIVGVVPEVPHDET 1115

QY 498 CDPAFLHVSNDYSFIRYTRTYQFOEALCQAAKHEGPHLKCDISNSTAGOKLFN 557  
DB 1116 FDPGSKFHPANVPYIRYFVSVFIQFQHQALCKAAGTGPLHTCDIYQSKAAGLLGD 1175

QY 558 LRLCKSEPTWTLALENVVGNKNNVRPLNLYFEPLTWLKDQNK--NSFVGW-STDWSP 612  
DB 1176 MGLGSKPEWPEAMKLIITGQPNMSASAMNYYFKELTEWLVTEENRRHGETLGPWPEYNAW 1233

RESULT 6  
JC2489  
peptidyl-dipeptidase A (BC 3.4.15.1) - chicken  
N:Alternate names: angiotensin converting enzyme  
C:Species: Gallus gallus (chicken)  
C:Date: 16-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 28-May-1999  
C:Accession: JC2489  
R:Bernstein, K.E.; Thomas Jr., K.E.; Bernstein, K.E.  
Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994  
A:Title: Chicken lacks the testis specific isozyme of angiotensin converting enzyme four

A:Reference number: JC2489; MUID:95110342; PMID:7811282

A:Accession: JC2489

A:Molecule type: mRNA

A:Residues: 1-1193 <EST>

A:Cross-references: GB:L40175; NID:G685169; PIDN:AAA75554.1; PID:G994708

C:Comment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase that cleaves a

C:Superfamily: mammalian peptidyl-dipeptidase A

C:Keywords: metal binding; peptidyl-dipeptide hydrolase; zinc

F:316,331,914,929/Binding site: zinc, catalytic (Glu, His, Glu, His) #status predicted

Query Match 30.6%; Score 1312; DB 2; Length 1193;

Best Local Similarity 40.4%; Pred. No. 2,7e-82;

Matches 264; Conservative 110; Mismatches 243; Indels 36; Gaps 10;

QY 22 EQAKTFLDKFHEADELFYQSSLASWNTNTITEENVQNMNAGDKWAFLEQSTLQ 81

DB 544 EAQAEFLSEYNSTAEVWNAYTEASWEYNTNITDHNKEVMDLEKVLAKSKHTIEVGMAR 603

QY 82 MYPLQEIQLTVKLOLQALQONGSSVLSDEKSKRLNTLNTMTSTYSGKVCNPN--P 138

DB 604 QDPSPDFQDETTRILNKLVLERAALPEDELKYNLLSDMETTYSVAKVCRENTHP 663

QY 139 QECLLEPGLNETMANSLDYNERLWAWESRSEVQKQLRPLVEEYVVLKNEVARANHYED 198

DB 664 -----LDPDLTDLATSRDYNELLFAWKGMWDASGAKTKOKRYVVELSKAAVLNGYTD 718

QY 199 YGDYWGDEYEVNGVDGYDSRGQLIEDVEHTFEEIKPLYLEHLHAYVRKLMNAY-PSYS 257

DB 719 NGAYWRSLEYETPFE-----EDLERLYQLQPLYLNLHAYVRRALYNKYGAHTS 768

QY 258 PIGCLPAHLGDMWGRFWTNLYSLTVFPQGNKPIDVTDMVDQAWDAQRIKFAEAKFFVS 317

DB 769 LKGPPIPAHLGDMWGRFWTNLYSLTVFPQGNKPIDVTDMVDQAWDAQRIKFAEAKFFVS 828

QY 318 VGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDL-GKGDPRILMCTKVMTDDFLTAHHEM 376

DB 829 LGLIPMPQEFWDKSMLEKADGREVWCHASAWDFYNRKDFRIKQCTVNVNMDLLITVHEM 888

QY 377 GHIQYDMAYAAQPLLRNGANEGHFAVEIGMSLSAATPKHLKSIIGLLSPDQEDNTEI 436

DB 889 GHVQYFLQYMDQPISTPRDGANPGFHEAIGDMWALSSTPKHLKSIINLLD-QVTENEESDI 947

QY 437 NFLLKQALTIIVGLTLPFTYMLEKRWVFKGEIPKQDMKKWEMKREIVGVVPEVPHDET 496

DB 948 NYLMSIALDKIAIFPFGYLMQWRKVFDRIRIKEDEYNQWNLRLKYQGLCPVPRSED 1007

QY 497 YCDPASLHVSNDYSFIRYTRTYQFOEALCQAAKHEGPHLKCDISNSTAGOKLFN 556

DB 1008 DFDPGAKFHPANVPYIRYFVSVFIQFQHQALCKAAGTGPLHTCDIYQSKAAGLLGD 1067

QY 557 MLRLCKSEPTWTLALENVVGNKNNVRPLNLYFEPLTWLKDQNK--KQNKNSFVGW-STDWSPY 613

DB 1068 AMKLGSKPEWPEAMKLIITGQPNMSAALMSYFPEPLTWLVKKTENGEVLGWEYSWTPY 1127

QY 614 ADQSIKVRISLSALG-----DKAYEWNENKYLFRSSVAVAMROYFLKVK 659

DB 1128 AVTEFHAATDADFLGMSVGTQKATAGW-----VLLALALAVLITISIFLGVK 1175

RESULT 7

JC2038

peptidyl-dipeptidase A (BC 3.4.15.1) - rat

N:Alternate names: angiotensin converting enzyme; kinase II

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: JC2038

R:Koike, G.; Krieger, J.E.; Jacob, H.J.; Mukoyama, M.; Pratt, R.E.; Dzau, V.J.

Biochem. Biophys. Res. Commun. 198, 380-386, 1994

A:Title: Angiotensin converting enzyme and genetic hypertension: Cloning of rat cDNAs

A:Reference number: JC2038; MUID:94121658; PMID:8292044

C:Accession: JC2038

A:Molecule type: mRNA

A:Residues: 1-1313 <KOI>



A:Accession: A60724  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 73-173 <SEN>  
R:Chen, Y.N.P.; Riordan, J.F.  
Biochemistry 29, 10493-10498, 1990  
A:Title: Identification of essential tyrosine and lysine residues in angiotensin converting enzyme isozyme  
A:Reference number: A36232; MUID:91104959; PMID:2176870  
A:Accession: A36232  
A:Molecule type: protein  
A:Residues: 154-160;236-242 <CHE>  
R:Iwata, K.; Lai, C.Y.; El-Dorri, H.A.; Soffer, R.L.  
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982  
A:Title: The NH2- and COOH-terminal sequences of the angiotensin-converting enzyme isozyme  
A:Reference number: A90107; MUID:83048249; PMID:6291514  
A:Accession: C18700  
A:Molecule type: protein  
A:Residues: 33-35, 'SN', '38-39', 'SS', 'FAEL', '737 <IWA>  
C:Comment: The pulmonary and testicular isoforms of this enzyme differ substantially in  
ggests that the two isoforms arise by alternative splicing of one gene.  
C:Superfamily: mammalian peptidyl-diesterase A  
C:Keywords: alternative splicing; peptidyl diesterase hydrolase; testis; transmembrane pr

Query Match 29.9%; Score 1283; DB 1; Length 737;  
Best Local Similarity 40.8%; Pred. No. 1.3e-80;  
Matches 250; Conservative 112; Mismatches 213; Indels 38; Gaps 10;

QY 20 TTEQAKTFLDKFHEADLIFYQSSLASWYNTNITEE-----NVQNMN--AGDKW 69  
DB 75 TDEASRFVEYDRSFQAVNVEAAENWYNTNITTEASKILLQKNMQIANHTLYGNW 134  
QY 70 SAFLKEQSTLAQMPLQEIQNITVKLOLQALQONGSVLSSEKSKELNTILMTSTIIS 129  
DB 135 -----ARRFVSNFQATSKRIIKVQDLQRAVLFPVKELEYNQLLDMETIYSV 184  
QY 130 GKVCNPDPQCLLEFGLANEIMANSIDYNERLWAMESWRSVEGKQLRPLYEYVVLKNE 189  
DB 185 ANVCRVDG - SCLQLEPDLTLMATSKYDELLWMTSWRDKVGRAILPVFPKYVEFTNK 242  
QY 190 MARANHEYDGYWRGDEYGVNGVDGYDSGQLIEQVEHTFBEIKELYEHLHAYYRAKLM 249  
DB 243 AARLNGYVDGDSWRSMTETPLB-----QDLERLFQELPLYLNLHAYYVGRALH 292  
QY 250 NAY - PSYISPIGCLPAHLGLDMGRFWNTLYSLTVPFGQKPNIDVTDMVDDQAWDAQRIF 308  
DB 293 RHYGAQHINLEGPIPAHLGLNMAQTSWNTSYDLVAPSPASMTDAEAMIKQGWTPRRMF 352  
QY 309 KEAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKG - DFRLLMCTKVMD 367  
DB 353 EADKFFLSGLLPVPFEPFNKSWLEKPTDREVVCHASANDFYNGKDFRIKQCTVYME 412  
QY 368 DELTAHEMNGHIQYDMAAYAAQPFLLRNGANGFHEAVEIMSLSATPRLKLSIGLLSPD 427  
DB 413 DLVWVHHMNGHIQYFMQYKOLPVALREGANPGFHEAIGDVLASVSTPKHLHSINLLSE 472  
QY 428 FQEDNETEINFLKQALITVGLTPFTMLEKVMWYFKGEIPKDWKKWKKWEMKREIVGV 487  
DB 473 -CGGYEHDLINFLKQALDKTAIFPSVLVDENWRVDFDSITKENYQWNSRLRYQGL 531  
QY 488 VEPVPHDETYCDPASLFHVSNDYSFIRYTRTYQFQFOEALCOAAKHEGPHLKCDISNS 547  
DB 532 CPAPRSQGFDPGAKFHIPSSVPIRYFVSFIQFQHEALCKAAGHTGPLHTCDIYOS 591  
QY 548 TEAGOKLFNMLRLGKSRFTWLALENVVGAKNMVRPLNLYFEPLFTWLKDQN - KNSFVG 605  
DB 592 KEAGKRLADAMKLGSPFWPEAMKVIITGQNNASASAMNYFPELMDLLITENGRGEKLG 651  
QY 606 W-STOWSPYADQS 617  
DB 652 WQPYTWTNSARS 664

RESULT 9  
S35484  
peptidyl-dipeptidase A (EC 3.4.15.1) precursor, pulmonary splice form - rabbit  
N;Alternate names: angiotensin-converting enzyme; dipeptidyl carboxypeptidase I; kininase  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: S35484; A23455; A18700; A38655; A49726; S17509  
R;Thakumara, T.J.; Livingston III, W.; Kumar, R.S.; Sen, G.C.  
Nucleic Acids Res. 20, 683-687, 1992  
A;Title: Use of alternative polyadenylation sites for tissue-specific transcription of the  
A;Reference number: S35484; MUID:92178960; PMID:1311831  
A;Accession: S35484  
A;Molecule type: mRNA  
A;Residues: 1-1309 <THE>  
A;Cross-references: EMBL:X62551  
R;Iwata, K.; Blacher, R.; Soffer, R.L.; Lai, C.Y.  
Arch. Biochem. Biophys. 227, 188-201, 1983  
A;Reference number: A23455; MUID:84051289; PMID:6314908  
A;Accession: A23455  
A;Molecule type: protein  
A;Residues: 34-47, 'N', 49-55 <IWA>  
A;Experimental source: lung  
R;Iwata, K.; Lai, C.Y.; El-Dorriy, H.A.; Soffer, R.L.  
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982  
A;Title: The NH2- and COOH-terminal sequences of the angiotensin-converting enzyme isozym  
A;Reference number: A90107; MUID:83048249; PMID:6291514  
A;Accession: A18700  
A;Molecule type: protein  
A;Residues: 34-44, 754-755, 'L', 757 <IW2>  
R;Kumara, R.S.; Thakumara, T.J.; Sen, G.C.  
J. Biol. Chem. 266, 3854-3862, 1991  
A;Title: The mRNAs encoding the two angiotensin-converting isozymes are transcribed from  
A;Reference number: A38655; MUID:91139683; PMID:1847388  
A;Accession: A38655  
A;Molecule type: DNA  
A;Residues: 1-88 <KUM>  
A;Cross-references: GB:M58579  
R;Ranchandran, R.; Sen, G.C.; Misano, K.; Sen, I.  
J. Biol. Chem. 269, 2125-2130, 1994  
A;Title: Regulated cleavage-secretion of the membrane-bound angiotensin-converting enzym  
A;Reference number: A49726; MUID:94124568; PMID:8294466  
A;Accession: A49726  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1236-1258 <RAM>  
A;Experimental source: testis  
R;Kirley, T.L.  
Biochem. J. 278, 375-380, 1991  
A;Title: The Mg(2+)-ATPase of rabbit skeletal-muscle transverse tubule is a highly glyco  
A;Reference number: S17509; MUID:91378880; PMID:1654880  
A;Accession: S17509  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 34-55 <KIR>  
C;Comment: This enzyme converts angiotensin I to angiotensin II in presence of divalent  
ver, the enzyme has been found also in renal tubules and intestinal mucosa.  
C;Superfamily: mammalian peptidyl-dipeptidase A  
C;Keywords: alternative splicing; blood pressure control; chloride; glycoprotein; intest  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;34-1309/Product: peptidyl-dipeptidase A, pulmonary #status experimental <MAT>  
F;59,79,150,322,448,512,680,698,717,945,1194/Binding site: carbohydrate (Asn) (covalent)  
Query Match 29.8%; Score 1283; DB 1; Length 1309;  
Best Local Similarity 40.8%; Pred. No. 3.1e-80;  
Matches 250; Conservative 112; Mismatches 213; Indels 38; Gaps 10;  
Qy 20 TIEQAKTFLDKFNHEADLFYQSSLASWNTNITEE-----NVQNMN--AGDKW 69  
Db 647 TDEAASRFEVEYDRGFQAVNWEAEANNWNTNITEASKILLQKNQIANHTLYGNW 706  
Qy 70 SAFLKEOSTLAQMPYQFQEQNLVTKLQALQNGSSVLSDEKSKRLNTILNTWNTIYST 129

Db 707 -----ARRFDVSNFQNAKSKRIKKYQDQLRAVLPVKELEYNQILLDMETIYSV 756  
Qy 130 GVCVNDPNEQECLELLEPCLEIMANSIDYNERLWAWSEWSEVKGQLRPLYEYVVLKNE 189  
Db 757 ANVCRVDG--SCLQLEPDLTWMATSKYIDELLVWTSWRDKVGRALPFPFKVETNK 814  
Qy 190 MARANHYEDGYWKGDEYVNGVDGYDSRGQLLEDVEHTFEETKPLYEHLHAYVRKLM 249  
Db 815 AARLNGYVDAGDSWRSWYETETLE-----QDLERLFOELQPLYLNLHAYVGRALH 864  
Qy 250 NAY-PSYISPIGCLPAHLGLDGMWGRFNTNLSLVTPFGQKPNIDVTDMYDQAWDAORIF 308  
Db 865 RHYGAHINLEGPIDPAHLGLGNWAGTWSNIYDVAFPSSASTMDATEAMIKQGTTPERP 924  
Qy 309 KEAEKFXVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKG--DFRILMCTKTMD 367  
Db 925 EADKFFISLGLLPVPPEFWNKSMLKPTDGRVYVCHASAWDFYNGKDFIKQCTTWNME 984  
Qy 368 DELTAHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSLGLLSPD 427  
Db 985 DLVVVHEMGHIQYDMAYKDLFVALREGANPGFHEAIGDVLALSVPKHLHSINLLSSE 1044  
Qy 428 FOEDNETEINFLKQALITVGLTLPFTYMLEKRWVFKGIPKQDQWKKWEMKREIVGV 487  
Db 1045 -GGYEHDFINFLKQWALDKIAFIPFSLVDEWRVRVFDGSIKENYNOEWSURLKYQGL 1103  
Qy 488 VEPVPHDETYCDPASLRFVSNIDYFIRYITRTLYQFQEQALCOAKHEGFLHKCDISNS 547  
Db 1104 CPPAPRSQDFFDPAKFFHPSVPIRVFVSFIQFQHEALCKAAGTGLHTCDIYQS 1163  
Qy 548 TEAGQKLFNMLRLGKSEPTWLALENVQAKMVRPLNLYPEPLFTWLKQDN--KNSFVG 605  
Db 1164 KEAGKELADAMKLGSKRPWPKAMVITGQPNMSASAMWYFKPLMDLLTENGHRHGEKJG 1223  
Qy 606 W-STDWSPYADQS 617  
Db 1224 WPQYTWTPNSARS 1236  
RESULT 10  
S65472  
peptidyl-dipeptidase A (EC 3.4.15.1) precursor - horn fly  
N;Alternate names: angiotensin I-converting enzyme  
C;Species: Haematobia irritans (horn fly)  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 22-Jun-1999  
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen,  
Eur. J. Biochem. 237, 414-423, 1996  
A;Title: Cloning and characterization of angiotensin-converting enzyme from the dipter.  
A;Reference number: S65431; MUID:96215437; PMID:8647080  
A;Accession: S65472  
A;Molecule type: DNA  
A;Residues: 1-611 <WIJ>  
A;Cross-references: EMBL:L43965; NID:G908759; PIDN:AAA70427.1; PID:G908760  
A;Note: the source is designated as Haematobia irritans exigua  
A;Accession: S65431  
A;Molecule type: protein  
A;Residues: 18, 'P', 20-42; 75-77, 'Q', 79-81, 'X', 83-84; 179-190 <WIW>  
A;Note: the source is designated as Haematobia irritans exigua  
C;Genetics:  
C;Superfamily: mammalian peptidyl-dipeptidase A  
C;Keywords: glycoprotein; metal binding; peptidyl-dipeptide hydrolase; zinc  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-611/Product: peptidyl-dipeptidase A #status predicted <MAT>  
F;53,196,531/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 24.7%; Score 1058; DB 2; Length 611;  
Best Local Similarity 37.2%; Pred. No. 3.5e-65;  
Matches 223; Conservative 108; Mismatches 246; Indels 22; Gaps 7;  
Qy 8 LLSLVAVTAQSTIEEQAKTFLDKFNHEADLFYQSSLASWNTNITEENVQNMNAGD 67

Db 8 ILAGLVACHGATKEEIVATEYELQINIKELAKHTNVTEVSWAYASNIITDENRLENSA 67  
 Qy 68 KWSAFLEKEOSTLAQMPLOEIQNLTVKQLQALQNGSSVLSSEKSKRLNTILNTMTIY 127  
 Db 68 ENAKFLKEVAKOIQKFNWYTGSDVRRQFKSLSTGYTSALPAEDYAEELLEVLGAMESNF 127  
 Qy 128 STGKVCNPNPOBC-LLLPGLNEIMANSLDYNERLMAWESWRSVGVKQLRPLVEEYVVL 186  
 Db 128 AKVRVCDYKNSAKCDLSLOPEIEEIIITKSRDPEELKYWTQPYDKAGTPTSRNFEKYVEL 187  
 Qy 187 KNEMARANYHEDYDGYWRGDEYVNGVDYDYSRGQLIED-VEHTFEEIKPLYEHLHAYR 245  
 Db 188 NTSKALNFTDGAENVLDEYE-----DATFEDQLEAIPEDIKPLYDQVHGVR 236  
 Qy 246 AKLMNAY-PSYISPIGCLPAHLGLDMWGRFNTNLSLTVPGQKFNIDVTDMYDQAWDA 304  
 Db 237 YRLNKFYGVDSVSKTGPLPMHLLGNMAQWSSIADIVSPPEKPLVDSDVEMVAQVTP 296  
 Qy 305 QRIFKEAEKFFVSVGLPNNTOGFWNSMLTDRGNVQKAVCHPTAWDLG-KGDFPILACTK 363  
 Db 297 LKWFQMGDDFFQSMGLKKLPQEFWDKSLDEKDDGRDLVCHASAWDFYLTDDVRIKQCTR 356  
 Qy 364 VTMDLFLTAHHEMGHIQYDMAYAAQFLLRNGANEGPHEAAGEIMSLSAATPKHLKISGL 423  
 Db 357 VTQDFEFTVHEHMGHIQYLOQHPFVYRTGANPGEHAGVDLSLSVSTPKELERVGL 416  
 Qy 424 LSPDFQEDNETEINFLLKQALITVGLTPTMYLXKRWMPKGEIPKDWKMKWEMKRE 483  
 Db 417 LK-NYVSDNEARINQLFTALDKIVLPFAFTMDKRYMSLFRGEYDKANMNCFAWKLREY 475  
 Qy 484 IGVWEPVPHDEYCDPASLPHVSNDSYFIRYRTLYQFOFQOALCOAA-----RHEG 537  
 Db 476 YSGIEPPVVRTEKDFDAPAKYHVSADVEYLRVLSFIIQFOFYKSACITAGIYVNPQTEY 535  
 Qy 538 PLHKCDISNSTEAGOKLFNMLRGLKSEFWTLALENVGAKMVRPLNLYPEPLFTWLK 596  
 Db 536 PLNCDIYGSKEAGKLFENMLSLGASKPWPDALEAFNGERTMTGKAIEYFEPRLVWLE 594

## RESULT 11

peptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (Drosophila melanogaster).  
 N;Alternate names: angiotensin-converting enzyme  
 C;Species: Drosophila melanogaster  
 C;Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 26-Feb-1998  
 C;Accession: A57533  
 R;Cornell, M.J.; Williams, T.A.; Lamango, N.S.; Coates, D.; Corvol, P.; Soubrier, F.; R  
 J. Biol. Chem. 270, 13613-13619, 1995  
 A;Title: Cloning and expression of an evolutionary conserved single-domain angiotensin d  
 A;Reference number: A57533; MUID:95293950; PMID:775412  
 A;Accession: A57533  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-615 <COR>  
 A;Cross-references: GB:U25344  
 C;Genetics:  
 A;Gene: FlyBase:Ance  
 A;Cross-references: FlyBase:FBgn0012037  
 C;Superfamily: mammalian peptidyl-dipeptidase A  
 C;Keywords: peptidyl-dipeptide hydrolase

Query Match 24.2%; Score 1039; DB 2; Length 615;  
 Best Local Similarity 35.8%; Pred. No. 7.3e-64;  
 Matches 219; Conservative 120; Mismatches 251; Indels 22; Gaps 9;  
 Qy 8 LLSLVAVTAQSTIEBQAKTFLDKFNHAEADLFYQSSLASWNYNTNTEENVQNNAGD 67  
 Db 8 LLATLAVTQALVKEIQAEYLENLKELAKRTNTEAAYGNSITDENKKNEISA 67  
 Qy 68 KWSAFLEKEOSTLAQMPLOEIQNLTVKQLQALQNGSSVLSSEKSKRLNTILNTMTIY 127  
 Db 68 ELAKFMKEVASDTTKQFQWSYQSEDUKRQFKALTKLGYAALFEDDYLAEELLDTLSGAMESNF 127

Qy 128 STGKVCNPNPOBC-LLLPGLNEIMANSLDYNERLMAWESWRSVGVKQLRPLVEEYVVL 186  
 Db 128 AKVRVCDYKNSAKCDLSLOPEIEEIIITKSRDPEELKYWTQPYDKAGTPTSRNFEKYVEL 187  
 Qy 187 KNEMARANYHEDYDGYWRGDEYVNGVDYDYSRGQLIED-VEHTFEEIKPLYEHLHAYR 246  
 Db 188 NTSKALNFTDGAENVLDEYE-----DATFEDQLEAIPEDIKPLYDQVHGVR 237  
 Qy 246 AKLMNAY-PSYISPIGCLPAHLGLDMWGRFNTNLSLTVPGQKFNIDVTDMYDQAWDA 305  
 Db 237 YRLNKFYGVDSVSKTGPLPMHLLGNMAQWSSIADIVSPPEKPLVDSDVEMVAQVTP 297  
 Qy 305 QRIFKEAEKFFVSVGLPNNTOGFWNSMLTDRGNVQKAVCHPTAWDLG-KGDFPILACTK 364  
 Db 297 LKWFQMGDDFFQSMGLKKLPQEFWDKSLDEKDDGRDLVCHASAWDFYLTDDVRIKQCTR 357  
 Qy 364 VTMDLFLTAHHEMGHIQYDMAYAAQFLLRNGANEGPHEAAGEIMSLSAATPKHLKISGL 424  
 Db 357 VTQDFEFTVHEHMGHIQYLOQHPFVYRTGANPGEHAGVDLSLSVSTPKELERVGL 417  
 Qy 424 LSPDFQEDNETEINFLLKQALITVGLTPTMYLXKRWMPKGEIPKDWKMKWEMKRE 484  
 Db 417 LK-NYVSDNEARINQLFTALDKIVLPFAFTMDKRYMSLFRGEYDKANMNCFAWKLREY 476  
 Qy 484 IGVWEPVPHDEYCDPASLPHVSNDSYFIRYRTLYQFOFQOALCOAA-----RHEG 538  
 Db 476 YSGIEPPVVRTEKDFDAPAKYHVSADVEYLRVLSFIIQFOFYKSACITAGIYVNPQTEY 536  
 Qy 538 PLHKCDISNSTEAGOKLFNMLRGLKSEFWTLALENVGAKMVRPLNLYPEPLFTWLK 598  
 Db 536 PLNCDIYGSKEAGKLFENMLSLGASKPWPDALEAFNGERTMTGKAIEYFEPRLVWLE 596  
 Qy 599 N-KNSFVGWST 608  
 Db 597 NTKNNVHIGWIT 608

## RESULT 12

JCS374

angiotensin-converting enzyme-related protein - fruit fly (Drosophila melanogaster)  
 C;Species: Drosophila melanogaster  
 C;Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jul-2000  
 C;Accession: JCS374  
 R;Taylor, C.A.M.; Coates, D.; Shirras, A.D.  
 Gene 181, 191-197, 1996  
 A;Title: The Acer gene of Drosophila codes for an angiotensin-converting enzyme homolog  
 A;Reference number: JCS374; MUID:97128790; PMID:8973330  
 A;Accession: JCS374  
 A;Molecule type: mRNA  
 A;Residues: 1-630 <TAY>  
 A;Cross-references: EMBL:X96913; NID:g1405881; PIDN:CAA65632.1; PID:g1405882  
 C;Genetics:  
 A;Gene: Acer  
 C;Superfamily: mammalian peptidyl-dipeptidase A

Query Match 24.0%; Score 1030; DB 2; Length 630;  
 Best Local Similarity 35.6%; Pred. No. 3.2e-63;  
 Matches 219; Conservative 113; Mismatches 260; Indels 24; Gaps 10;

Qy 6 WLLSLVAVTAQSTIEBQAKTFLDKFNHAEADLFYQSSLASWNYNTNTEENVQNNNA 65  
 Db 16 WLPGLSGNCSASVLE-ARRFELENEQLRRRFEELSGYNYNTNTEANQAMIEV 74  
 Qy 66 GDKWSAFLEKEOSTLAQMPLOEIQNLTVKQLQALQNGSSVLSSEKSKRLNTILNTMT 125  
 Db 75 YARNAELNKLRAQQTICKSSDYQSEDAIRRQAEHLKLGASALNADDYALQALQAISSMQT 134  
 Qy 126 IYSTGKVCNPNPOBC-LLLPGLNEIMANSLDYNERLMAWESWRSVGVKQLRPLVEEYV 184  
 Db 135 NYATATVCSYTRSDCSLTLEPHIQERLSHRDPAELAWYRWHDKSGTFPMQNFAYV 194  
 Qy 185 VLKNEARANYHEDYDGYWRGDEYVNGVDYDYSRGQLIED-VEHTFEEIKPLYEHLHAYV 244

Db 195 RLTRKASQLNGHRSYADYVWVQFYB-----DPDFER-----QLDATEKQLPLPLYRLHGVV 244  
 QY 245 RAKLMNAY-PSYISPIGCLPAHLGDMGFRWNLYSLTVPPGQKKNIDVTAMVDQAWD 303  
 Db 245 RFRIRQHYGPDVMPAEGNIPISLGNMWSWNLDELFTPYEPKFPVDVKAEMKQGYT 304  
 QY 304 AQRIFKBAEKFFSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCT 362  
 Db 305 VOKLFELGDQFFQSLGRALPPSPWNLVLTDPD-RQVVCHASANDVFDQSDVRIKMT 363  
 QY 363 KVTWDDDELTAHENGCHTOYDAYAQAOPFLRNGANGFHEAVEIMSLSAATPKHLKSG 422  
 Db 364 EVDGSHFYVHHEIGHIOYLYQVSEQQPAVYRGAPNPGFHEAVGDVIALSVMSAKHLKAIG 423  
 QY 423 LLSPDFQEDNTEINFLKQALITVGLPFTYMLKRWMMVFGEIPEKQWMMKQWEMKR 482  
 Db 424 LIE-NGLRDEKSRINQLFKQALSIVFLPFGYAVDYKYAVAFVFNELDEQWNGCFWOMBS 482  
 QY 483 EIVGVPEVPVPHDETCYPASIFHVSNDYSFIRYTRTLQFOQOEALCOAAKEGP-----538  
 Db 483 EFGGVEPPVFTTEKDFDPPAKYHIDADVYIRFAAHIFQFQHKVLCRRAGQYAPNNGR 542  
 QY 539 --LHKCDISNSTEAGQKFLNMLRGKSEPTWLTALENVGAKNNVRLNLYPERLFTWLK 596  
 Db 543 LTLNCDIFGSKAAGRSLSQFLSKGNSRHWKEVLEFTGETEMDPAALLEYPERLYQWLK 602  
 QY 597 DQNKNSFVGWSTWSP 612  
 Db 603 QE--NSRLGVPLGWP 616

## RESULT 13

T15792  
 C:Species: Caenorhabditis elegans  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000  
 C:Accession: T15792  
 R:Hallsworth, K.  
 Submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of C. elegans cosmid C42D8.  
 A:Reference number: 218405  
 A:Accession: T15792  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-907 <HAL>  
 A:Cross-references: ENBL:U56966; NID:g1293844; PID:g1293847; PIDN:AAA98719.1; GSPDB:GN00  
 A:Experimental source: strain Bristol N2; clone C42D8  
 C:Genetics:  
 A:Map position: X  
 A:Introns: 140/3; 170/3; 194/3; 300/2; 467/3; 551/2; 600/2; 697/3; 774/2; 851/3

Query Match 15.0%; Score 642.5; DB 2; Length 907;  
 Best Local Similarity 27.0%; Pred. No. 3.5e-36;  
 Matches 172; Conservative 136; Mismatches 289; Indels 41; Gaps 19;  
 QY 2 SSSWLLSLVAVTAAGSTIEQAKTFLDRFNHEADLFYQSSLASWNYNTNITEENVON 61  
 Db 160 SSNYWKTDLQAPGSIKD--BEKLSWLAGYEAIAKVLREVALSGWRYFNDASPSLKA 217  
 QY 62 MNNAGDKWSAFLKQSTLAQMYPLQIQLTVKQLQALQONGSSVLSEDKSKRLNTILN 121  
 Db 218 LDEAVLTMVFRSTSMQAKQFDMASVTDEKWRQLGYVSEFGSALAFSRFADYSQAQA 277  
 QY 122 TWSTYISGKVCNPNPQECLELLPEGLNEINANSLDYNERLWAWESWRSEVKGQLRPLYE 181  
 Db 278 ALNRDSKDSSTICDKDVPPCALQIDMDSIFRNEKQASRLQHLWVSVYTAIAKS-KPSYN 336  
 QY 182 EYVVLKNSMARANYEDYGVWRGDYVNG-VDCGYDSRGQLIEDVEHTFEETKPLYEHL 240  
 Db 337 NIITISNGAKLNGFANGAMWSAFDMSKVKHAEF---DLNKQDKYISITQPPYQL 393  
 QY 241 HAYVRKLMNAY--PSYISPIGCLPAHLGDMGFRWNLYSLTVPPGQKKNIDVTAMV 298

Db 394 HAYMRQLAGISYNPVGLSKOGPIPAHLFGSLDGDWNAHYEQTKPFEESS--ETPEAWL 451  
 QY 299 D-----QAWDAQRIFKBAEKFFSVGLPNNMTQGFWNSMLTDPGNVQKAVCHP-TAWDL-G 352  
 Db 452 SAFNTQNTYTKMFMFTVAYRYFKSAGPPLPKSYNTSSIFARVWS-KDMICHIPAAALDWA 510  
 QY 353 KGDPRILMCTKVTMDDELTAHENGHIQYDMAYAAQAPFLRNGANGFHEAVEIMSLSA 412  
 Db 511 PNDFRVKAQALGEPDFEQAHSLLVQTYQYLYKQOSLLFREQASPVITDAIANAPAHLS 570  
 QY 413 ATPKHLKSGICLLSPDPQEDNETE-INFLKQALITVGLTPTTYMLKRWMMVFGEIPEK 471  
 Db 571 TNPHYLYSQKLVSEHLIDKDSVIIKLYKESLEFTKLPTTIAADNNRYELDFDGTVEKN 630  
 QY 472 QWKKKWMEMKREIVGVVEVPVPHDETCYPASLFH--VSNDSYFIRYTRTL-----YQPF 525  
 Db 631 KLNDRWWEIRNKYEGVRSQPNTSNLD--ALHNSVSQVHS---PATRTLLISVYLKQI 685  
 QY 526 QBALCOAA---KIEGPHLHKDISNSTEAGQKFLNMLRGKSEPTWLTALENVGAKNNVR 582  
 Db 686 LKALCORELFWLSEG----CILSEDTT--EKURETMKLGSSITWLKALEMISGKELDAQ 739  
 QY 583 PLLNYPELFTMLKQNK--NSFVGWSTWSPYADQSI 618  
 Db 740 PLLEYEPLINLNRNTNEIDQVVVGWGDGEGTFTVEEI 777

## RESULT 14

C83696  
 C:Species: Bacillus halodurans  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 C:Accession: C83696  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, N.; Fujii, F.; Hii  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 Article: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A:Reference number: A83650; MUID:20512562; PMID:11058132  
 A:Accession: C83696  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-532 <STO>  
 A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA04090.1; GSPDB:GN  
 A:Experimental source: strain C-125  
 C:Genetics:  
 A:Gene: BH0371

Query Match 3.7%; Score 157; DB 2; Length 532;  
 Best Local Similarity 21.1%; Pred. No. 0.0058;  
 Matches 118; Conservative 83; Mismatches 213; Indels 144; Gaps 29;  
 QY 22 EQAKTFLDRFNHEADLFYQSSLASWNYNTNITEE-NVQNNNAGDKWSAFLKQS---77  
 Db 3 EQDIERFLSQNRKVEDLYQPVLLNHWVATTGGEWSDKHEQSLEYWAWHFSDESQK 62  
 QY 78 -----TLAQMYPLQIQLTVKQLQALQONGSSVLSEDKSKRLNTILNTMTYI 127  
 Db 63 VTRFRKIDSPLMQRRQLDLDDHKMTKQFE--EGTQOILSLE--KKISHVFTTFQPV 118  
 QY 128 STGVKCNPNPQECLELLPEGLNEINANSLDYNERLWAWESWRSEVKGQLRPLYEYVVLK 187  
 Db 119 NGRVSNNE-----LLDILRYDLDRERKQAWFA-SKEVGKTEKDLQLIRK 166  
 QY 188 NEWARNHYEDYGVWRGDYVNGVDCGYDSRGQLIEDVEHT---FEIKPIYEHLYAV 244  
 Db 167 NEVARNLGFTF-----YHMSFATQELDEQFAMFETIKKSSDQAFRMI 211  
 QY 245 -----RAKLMNAYPSYISPIGCLPAHLGDMGFRWNLYSLTVPPGQK-PNIDVTDA 296  
 Db 212 KBEIDERAKVZIKKDDLRP-----WDYDPPFPQEPAPSEHYD- 250  
 QY 297 MYDQAWDAQRIKFAEKFFSVGLPNNMTQGFWNSMLTDPGNVQK-AVCHPTAWDLGKGD 355

Db	251	-PDSFYKQDLQEVVSVQTFQAMLP---IDDLKSGSLYPRKNKNPFQFC--TDMD-RRGD	304
Qy	356	FRILMCTKVMTDDFLTAHEMGH-IQYDMAYAAQPELLNGANEGPHEAVGEIMSLSAT	414
Db	305	IRVLLNDQSMVWVTALLHEFGHAVYFKFIDSRLEPFLR-----PH-----SHTLTT	351
Qy	415	PKHLKSIGLLS--PDFOE-----DNET-----EINFLKQALITVITLPTFYMLEKWRW	461
Db	352	EASALPFGMTKNAEYVERPLGDRTCRIGRNMEKMLQRM-VVST-----RW	400
Qy	462	MV-----FKG---BIPKQDKMKWEMKREIVGVVEPHDETYCDPASLFHVS-----N	508
Db	401	MLAFSPFEKSLYEDPDQDINALMWKLVKIQYMAP--PEDTGSDDWAARHFLAPVYVQ	458
Qy	509	DY-----SFIRYVTRT	519
Db	459	DYLLGEMASQLHYIKT	476
RESULT 15			
AF1310			
probable thermostable carboxypeptidases homolog lmo1886 [imported] - Listeria monocytogenes			
C;Species: Listeria monocytogenes			
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001			
C;Accession: AF1310			
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.			
Science 294, 849-852, 2001			
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.			
A;Reference number: AB1077; MUID:21537279; PMID:11679669			
A;Accession: AF1310			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-502 <GLA>			
A;Cross-references: GB:NC_003210; PIDN:CAC99964.1; PID:g16411339; GSPDB:GN00177			
A;Experimental source: strain EGD-e			
C;Genetics:			
A;Gene: lmo1886			
C;Superfamily: Thermus aquaticus carboxypeptidase Taq			
Query Match 3.6%; Score 154; DB 2; Length 502;			
Best Local Similarity 20.1%; Pred. No. 0.0085;			
Matches 128; Conservative 101; Mismatches 215; Indels 192; Gaps 35;			
Qy	20	TIEQAKTFLLDKFNHEADLFYQSSLASWNYNT-----NITEENVQNNNA	65
Db	4	TLEEFLLAYIKKMEALREAL-----ALVYVDLRTGAPAKMGERSDVGVLSEEIFNNQTS	59
Qy	66	GDKWSAFLKEOSTLAQMYPLQEIQNLTKLQALQONGSSVLSEDSKSL-----N	117
Db	60	-EEMAAFTAGLN-----QDKENLS-EITRKTLEE---SQKTYDLNKKIPKEYAEYT	106
Qy	118	TILNTMTSTYTGKVCNPDNPQECLELLEPGLEINMANSLDYNERLWAWESWRSEVKGQLR	177
Db	107	KLVAQAETAWTAREQN-----DFAAFEPFLTKIL-----	136
Qy	178	PLYEYVVLKNEMARANHVEDYDGRGDYEVNGVDGY--DYSRGQLIEDVHETFEIKP	235
Db	137	-----EMKR-----KFVEYV--GYEENKYDTLLDQYEPGVTVSVLDSVFEKVR--	177
Qy	236	LYEHLHAYVRAKLNNAYPSYISPIGCLPAHLGDMWGRFTNLYSLTVPFQCKPNIDVTD	295
Db	178	--DGIMA-IREKIENE-----GVKPDATILN	200
Qy	236	AMVDQAWDAQRIKFAEKEFFVSGLPNTQGFWNSMLTDRGNVQKAVCHPTAMDGLKGD	355
Db	201	TKISEA-----KQKEFSIRI-LNKGDFD-----EAGRLDET-VHFAATGLNTGD	243
Qy	356	PRILMCTKVMTDDFLTA-----HHEMGIQY-----DMAYAAQFFLIRNGANEGPHEAVG--	405

Db	244	VRI--TTRYNENDFKMAVFGTIIHEGGHAIYEQNFDAAALVGTP--LANGASMGIHESQSLF	299
Qy	406	-EIM---SLSAATPKHLKSTGLLSPDFQ-----ED-----NETEINFLKQALITVGTLP-	451
Db	300	YEIIIGSSLAFWKSNYADFOAITKPAFDQVKLEDFYRAVNISESSLIRIEADTL--TYPL	357
Qy	452	---PTYMLEKRWMMVFKEBIPKQOMKQWEMKREIVGVVEPHDETYCDPASLFHVS	508
Db	358	HIMIRYELEK---ALINGELEVKDLKPAWGDKYEEYLG---RFDNDTNGVLQDIHWAGG	411
Qy	509	DYSFIRYVTRTL-YQFOFQBALCOAAKHEGLHKHCIDISNSTEAGQKLF---NMLRLGKSE	564
Db	412	DFGYFPYSALGLMYAAQFFNQM-----QKEIPNIDAILIASDDYSELKIMLIEHVHKFGKTK	467
Qy	565	PWTALLENVVGAKNNVRPLNLNYPEPLFTWLKDQNK	600
Db	468	KPLEILDTTIG-EGLNPTYLLDLLEKRYAYVYQFNK	502

Search completed: February 19, 2004, 19:51:41  
Job time : 25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 19, 2004, 19:44:13 ; Search time 17 Seconds  
(without alignments)  
2226.853 Million cell updates/sec

Title: US-09-163-648-2

Perfect score: 4291

Sequence: 1 MSSSSWLLSLVAVTAAQST.....ISKGNPFQNTDVTQSF 805

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1344	31.3	732	1 ACET_HUMAN	P22966 homo sapien
2	1337	31.2	1306	1 ACE_HUMAN	P12821 homo sapien
3	1334	31.1	732	1 ACET_MOUSE	P22967 mus musculus
4	1334	31.1	1312	1 ACE_MOUSE	P09470 mus musculus
5	1312	30.6	1193	1 ACE_CHICK	Q10751 gallus gall
6	1310	30.5	1313	1 ACE_RAT	P47820 rattus norv
7	1283.5	29.9	1310	1 ACE_RABIT	P12822 coryctolagus
8	1283	29.9	737	1 ACET_RABIT	P22968 coryctolagus
9	1085	25.3	615	1 ACE_DROME	Q10714 drosophila
10	1058	24.7	611	1 ACE_HAIE	Q10715 haematobia
11	135	3.1	501	1 YPWA_BACSU	P50848 bacillus su
12	125	2.9	627	1 GLGB_BACSU	P39118 bacillus su
13	123	2.9	986	1 EP1B_STABP	P30195 staphylococ
14	121	2.8	1034	1 BGAL_BACME	O52847 bacillus me
15	119.5	2.8	1283	1 OSH2_YEAST	Q12451 saccharomyc
16	119.5	2.8	3655	1 YAMB_SCHPO	Q10064 schizosacch
17	119.5	2.8	4540	1 DYHC_PART	Q27171 paramesium
18	118	2.7	663	1 NTHR_CABEL	Q17693 caenorhabdi
19	118	2.7	1826	1 K13B_HUMAN	Q9ngt8 homo sapien
20	118	2.7	3911	1 AXA9_HUMAN	Q99996 h a-kinase
21	115.5	2.7	3433	1 UTR0_HUMAN	P46939 homo sapien
22	115	2.7	950	1 Y511_RICPR	Q9zd36 rickettsia
23	114.5	2.7	901	1 PIP_YACLA	P49022 lactococcus
24	114.5	2.7	1225	1 Y309_MYCGE	P47551 mycoplasma
25	114	2.7	1284	1 CWFB_SCHPO	O94508 schizosacch
26	113.5	2.6	6669	1 NEBU_HUMAN	P20929 homo sapien
27	113	2.6	638	1 SYM_THETN	Q8rd01 thermocanaer
28	113	2.6	6885	1 SNE2_HUMAN	Q8wxh0 homo sapien
29	112.5	2.6	773	1 CBH_FHACH	Q01738 phaeocrohae
30	112.5	2.6	782	1 OSTA_PASMU	Q8ck12 pasteurella
31	110	2.6	660	1 SYM_BACHD	Q9kgk8 bacillus ha
32	109.5	2.6	1398	1 DNA2_SCHPO	Q9uruz schizosacch
33	109	2.5	906	1 Y010_CLOAB	Q97n28 clostridium

## ALIGNMENTS

### RESULT 1

ID	ACET_HUMAN	STANDARD;	PRT;	732 AA.
AC	P22966;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Angiotensin-converting enzyme, testis-specific isoform precursor			
DE	(EC 3.4.15.1) (ACE-T) (Dipeptidyl carboxypeptidase I) (Kininase II).			
GN	ACE OR DCPI OR DCP			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90046671; PubMed=2554286;			
RA	Ehlers M.R.W., Fox E.A., Strydom D.J., Riordan J.F.;			
RT	"Molecular cloning of human testicular angiotensin-converting enzyme;			
RT	the testis isozyme is identical to the C-terminal half of endothelial			
RT	angiotensin-converting enzyme.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:7741-7745 (1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89338720; PubMed=2547653;			
RA	Lattion A.L., Soubrier F., Allegrini J., Hubert C., Corvol P.,			
RA	Alhenc-Gelas F.;			
RT	"The testicular transcript of the angiotensin I-converting enzyme			
RT	encodes for the ancestral, non-duplicated form of the enzyme.";			
RL	FEBS Lett. 252:99-104 (1989).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANTS PRO-32; GLY-49 AND SER-712.			
RX	MEDLINE=99251980; PubMed=10319862;			
RA	Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;			
RT	"Sequence variation in the human angiotensin converting enzyme.";			
RL	Nat. Genet. 22:59-62 (1999).			
RN	[4]			
RP	ZINC-BINDING.			
RX	MEDLINE=91308093; PubMed=1649623;			
RA	Ehlers M.R., Riordan J.F.;			
RT	"Angiotensin-converting enzyme: zinc- and inhibitor-binding			
RT	stoichiometries of the somatic and testis isozymes.";			
RL	Biochemistry 30:7118-7126 (1991).			
RN	[5]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=96302256; PubMed=8755737;			
RA	Sturrock E.D., Yu X.C., Wu Z., Biemann K., Riordan J.F.;			
RT	"Assignment of free and disulfide-bonded cysteine residues in testis			
RT	angiotensin-converting enzyme: functional implications.";			
RL	Biochemistry 35:9560-9566 (1996).			
CC	!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF			
CC	THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE			
CC	VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN. ALSO ABLE TO INACTIVATE			
CC	BRADYKININ, A POTENT VASODILATOR.			
CC	!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,			
CC	oligopeptide-[Xaa-Xbb, when Xaa is not Pro, and Xbb is neither			

P30822 saccharomyc  
P25356 saccharomyc  
P15398 schizosacch  
P11532 homo sapien  
P26193 porcine rot  
P12753 saccharomyc  
Q13017 homo sapien  
O50314 chlorobium  
P57654 buchnera ap  
P24740 human immun  
Q89a93 buchnera ap  
P38903 saccharomyc

34 108.5 2.5 1084 1 XPO1\_YEAST  
35 108.5 2.5 2167 1 BP11\_YEAST  
36 107.5 2.5 1689 1 RP11\_SCHPO  
37 107.5 2.5 3685 1 DMD\_HUMAN  
38 107 736 1 VP4\_ROTPE  
39 106.5 2.5 1312 1 P450\_YEAST  
40 106.5 2.5 1499 1 RHGS\_HUMAN  
41 106 2.5 1279 1 BCHKI\_CHLVI  
42 105.5 2.5 645 1 REP\_BUCAI  
43 105.5 2.5 1002 1 POL\_HV1U4  
44 105 2.4 626 1 HTPG\_BUCBP  
45 104.5 2.4 757 1 P450\_YEAST

FT	VARIANT	722	722	Q -> P (IN dbSNP:4981).
ST	SEQUENCE	732 AA; 83330 MW; 80E0D19CFA642313 CRC64;		/FTID-VAR_014741
SQL	Query Match	31.3%; Score 1344; DB 1; Length 732;		
	Best Local Similarity	41.8%; Pred. No. 8.4e-87;		
	Matches 259; Conservative	119; Mismatches 204; Indels 38; Gaps 10;		
QY	15	TAAGS----	TIEGAKTFLDKFNHEAEDLFYGOSSLASWNYNTNITEE-----NVQNM 62	
DB	61	TSAGSNLVTDEAFSAKFVEYDRTSOVWNEVAEANYNYNTIT	TSTSKILLQKNQIA 120	
QY	63	NNAGKWSAFKEOSTLAQMYPIQETQNTLVKLQALQOQNGSSVL	SDSKSLNTILNT 122	
DB	121	NHT-----LKYGTQARKFDVNOQNTTIKRIIKVODLERAAP	QAEUEYNKILLD 172	
QY	123	MSITYSTGKVCNPNQECILLPEGLNEIMANSLDYNERLMAWES	WRSEVGKQLRPLYEE 182	
DB	173	METYSYVATVCHPNG--SCLQEPDLTNYMATSRYKEDLLWA	EGWRDKAGRAILQFPYK 230	
QY	183	YVVLKNEVARANHYEDVDYWRGDYEVNGVDYDSRGQLIED	VHTTEIKPLVEHLHA 242	
DB	231	YVELINOARLINGYVDAGDSWRSMYETPSLE-----QDL	ERLQFQLQPLYLHLA 280	
QY	243	YVRAKLMNAY--PSVTSIPGCLFAHLLCDMMGRFTWNTLY	SLTFPGOKPNIDVTDAMVQA 301	
DB	281	YVRALHRYGAQHINLEGPIFAHLLGNMWAQTSNIYDLV	VFFTSAPSMDTTEAMLKQG 340	
QY	302	WDAQIFYEAKKFFVSVGLPNMTGCFWENSMITDPGNVQK	AVCHPTAWDLGKG-DFRILM 360	
DB	341	WTPREMFKEAADFTSLGLLVPPEPFWNKSMLEKPIDG	REVVCASANDFYNGKDFRIKQ 400	
QY	361	CTKWMTMDFLTAHHEMGHIQYDMAAQAQPELLRANGANE	GFEHVAVGSEIMSLSAATPKHLKS 420	
DB	401	CITVWLEDLVVAHEMGHIQYFMQYKDLPVALREGANPG	FHEAIGDVLALSYSTPKHLHS 460	
QY	421	IGLLSPDFQEDNEITEINFLKQALTI VGTLPFTYMLEK	WVYFKEGEPKIDQWKKWEM 480	
DB	461	INLLSEGGSD--EHDINFEMKALDKIAFIPFSLVDQWR	VFDGSIYKENYNGEWSL 519	
QY	481	KREIVGWVEVPVPHDTCYDPAFLSHFVSNDSYFIRYTR	TLYQFQFQALCOAKHEGPIH 540	
DB	520	RLKYQGLCPFPVPTQDGPDAKEHIPSSVPYIRYFVS	FIQPFQFHEALCOAGHTGPIH 579	
QY	541	KCDISNSTAGOKLFWMLRLGKSEBPTALENVGAKNM	VRLNVPFLNVPFLTWLQDNK 600	
DB	580	KCDIYQSKAGORLATANKLGFSPRPWEMQLITGQFN	MSASANLSYFKPELLDLNLTENE 639	
QY	601	--NSFPYGV--STDWSPYADQS 617		
DB	640	LHGEKLGWPQYNWTFNSARS 659		
	RESULT 2			
	ACE HUMAN			
ID	ACE HUMAN	STANDARD;	PRT; 1306 AA.	
AC	P12821;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)			
DE	(ACE) (Dipeptidyl carboxypeptidase I) (Kininase II) (CD143 antigen).			
GN	ACE OR DCP1 OR DCP.			
OS	Home sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89071703; PubMed=2849100;			
RA	Soubrier F., Alenc-Gelas F., Hubert C., Allegrini J., John M.,			
RA	Tregear G., Corbol P.;			
RT	"Two putative active centers in human angiotensin I-converting enzyme			

RT revealed by molecular cloning.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:9386-9390 (1988).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANTS SER-261; TRP-561 AND SER-1286.  
RX MEDLINE=99251580; PubMed=10319862;  
RA Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;  
RT "Sequence variation in the human angiotensin converting enzyme.";  
RL Nat. Genet. 22:59-62 (1999).  
RN [3]  
RP PARTIAL SEQUENCE OF 30-46.  
RC TISSUE=Lung;  
RX MEDLINE=90110025; PubMed=2558109;  
RA Takeuchi K., Shimizu T., Ohishi N., Seyama Y., Takaku F.,  
RY Yotsumoto H.;  
RT "Purification of human lung angiotensin-converting enzyme by high-performance liquid chromatography: properties and N-terminal amino acid sequence.";  
RL J. Biochem. 106:442-445 (1989).  
RN [4]  
RP ZINC-BINDING.  
RX MEDLINE=91308093; PubMed=1649623;  
RA Ehlers M.R., Riordan J.F.;  
RT "Angiotensin-converting enzyme: zinc- and inhibitor-binding stoichiometries of the somatic and testis isozymes.";  
RL Biochemistry 30:7118-7126 (1991).  
RN [5]  
RP VARIANTS THR-1018; VAL-1051; GLN-1279; SER-1286 AND PRO-1296.  
RX MEDLINE=99318094; PubMed=10391210;  
RA Halushka M.K., Ran J.-B., Bentley K., Haie L., Shen N., Weder A.,  
RY Cooper R., Lipshutz R., Chakravarti A.;  
RT "Patterns of single-nucleotide polymorphisms in candidate genes for blood-pressure homeostasis.";  
RL Nat. Genet. 22:239-247 (1999).  
RN [6]  
RP FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN. ALSO ABLE TO INACTIVATE BRADYKININ A POTENT VASODILATOR.  
CC -! CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide.|-Xaa-Xbb, when xaa is not pro, and xbb is neither asp nor glu. Converts angiotensin I to angiotensin II.  
QC -! COPACITOR: Binds 2 zinc ions (By similarity).  
CC -! SUBCELLULAR LOCATION: Type I membrane protein.  
CC -! ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=Somatic;  
CC IsoId=PI2821-1; Sequence=Displayed;  
CC Name=Testis-specific;  
CC IsoId=P22966-1; Sequence=External;  
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.  
CC -! DATABASE: NAME=PRO; NOTE=CD guide CD143 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd143.htm".  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; J04144; AAA51684.1; -;  
DR EMBL; AF118569; RAD28560.1; -;  
DR PIR; A31759; A31759.  
DR MEROPS; M02.001; -;  
DR MEROPS; M02.004; -;  
DR Genew; HGNC:2707; ACE.  
DR MIM; 106180; -;  
DR GO; GO:0005624; C:membrane fraction; TAS.  
DR GO; GO:0005886; C:plasma membrane; TAS.  
DR GO; GO:0005625; C:soluble fraction; TAS.  
DR GO; GO:0008217; P:regulation of blood pressure; TAS.  
DR InterPro; IPR001548; Peptidase\_M2.  
DR InterPro; IPR006025; Zn\_MTPeptide.

DR pfam: PF01401; Peptidase\_M2; 2.  
DR PRINTS; PR00791; PEPTIDPASE.  
DR ProDom; PD004184; Peptidase\_M2; 2.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 2.  
KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;  
KW Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing;  
KW Polymorphism.  
FT SIGNAL 1 29 ANGIOTENSIN-CONVERTING ENZYME, SOMATIC  
FT CHAIN 30 1306 ISOFORM.  
FT DOMAIN 30 1259 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1260 1276 POTENTIAL.  
FT DOMAIN 1277 1306 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 227 583  
FT REPEAT 825 1181  
FT METAL 390 390  
FT ACT SITE 391 391  
FT METAL 394 394  
FT METAL 988 988  
FT ACT SITE 989 989  
FT METAL 992 992  
FT METAL 992 992  
FT CARBOHYD 38 38  
FT CARBOHYD 54 54  
FT CARBOHYD 74 74  
FT CARBOHYD 79 79  
FT CARBOHYD 111 111  
FT CARBOHYD 146 146  
FT CARBOHYD 160 160  
FT CARBOHYD 272 272  
FT CARBOHYD 318 318  
FT CARBOHYD 445 445  
FT CARBOHYD 509 509  
FT CARBOHYD 677 677  
FT CARBOHYD 695 695  
FT CARBOHYD 714 714  
FT CARBOHYD 760 760  
FT CARBOHYD 942 942  
FT CARBOHYD 1191 1191  
FT VARIANT 261 261  
FT VARIANT 561 561  
FT VARIANT 1018 1018  
FT VARIANT 1051 1051  
FT VARIANT 1279 1279  
FT VARIANT 1286 1286  
FT VARIANT 1296 1296  
FT CONFLICT 35 35  
FT CONFLICT 42 42  
FT CONFLICT 1306 AA; 149714 MW; 1B39BCA7301A268A CRC64;  
SQ SEQUENCE 1306 AA; 149714 MW; 1B39BCA7301A268A CRC64;  
Query Match 31.2%; Score 1337; DB 1; Length 1306;  
Best Local Similarity 41.7%; Pred. No. 6.1e-86;  
Matches 255; Conservative 118; Mismatches 204; Indels 34; Gaps 9;  
QY 20 TIEQAKTFLDKENHEAEDLFYQSSIASNNYNTITEE-----NVQNMNAGDKWSA 71  
DB 644 TDEAEASKFVEEYDRTSQVWNEAYANNNYNTITEE-----SKILLQKNQIAHNT----- 697  
QY 72 FLKEQSTLAQMPLOEIQNLTKVLQLOALQOQNGSSVLSEDKSKRLNTILNTWTSTYSTOK 131  
DB 698 --LKYGTQARKFDVNLQNTTKRIKKYQDLERAPALPAQELEYVKNILLDMETYSVAT 755  
QY 132 VCNPDNPQECILLLEPGINIMANSLDNERLWAWESWRSEVGKQLRPLVEEYVLLKNEWA 191  
DB 756 VCHENG--SCLQLEPDLTNVMTATSRKYEDLLWAWEGWRDKAGRAILQFPKVELINQAA 813  
QY 192 RANHYEDYGDYWRGDEYVNGVDYDYSRGQLIEDVEHTFEIKPLYEHLHAYVRAKLMNA 251



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Db 814 RLNGYVDAGSWMRYETPSLE-----ODLERUFQELQPLYLNLHAYVRAALRH 863
Qy 252 Y-PSYISPIGCLPAHLGLGMDGWFNLYSLVFPQKPNIDVTAMDVDQAWDAQRIKFE 310
Db 864 YGAQHINLEGPIDAHLLGNNAWQTSNIYDLVVPFAPSMDTTEAMLKQGTWTRMFKE 923
Qy 311 AEKFFSVGLPNNQTFWNSMLTDPGNTOKAVCHPTAWDLGK-DEFLMCTVMTWDDP 369
Db 924 ADDFFSLGLPLPVPFPPFNKSMLEKETDGREVVCCASAWDFYNGKDFRIKCTTNNLEDL 983
Qy 370 LTAHHEHGHIIQYDWAYAAQFLLRNGANEGFHEAVGEIMSLSAATPKHLKSLGLSPDFQ 429
Db 984 VWAHHEHGHIIQYDWAYAAQFLLRNGANEGFHEAVGEIMSLSAATPKHLKSLGLSPDFQ 1043
Qy 430 EDNETETNELLKALATVGLTPPTMYLXKRWMPKGEIPKDDWKKWKKMKREIVGVVE 489
Db 1044 SD-EHDINFLMKWALDKIAFIPSYLVQWRVRVFGSTIKENYQEWWSRLKXVGLCP 1102
Qy 490 PVPHETPCDPSLPHVNSDYSIRYTRTLVQFQFQALCOAAKHGELHKKDISNSTE 549
Db 1103 PVPHETPCDPSLPHVNSDYSIRYTRTLVQFQFQALCOAAKHGELHKKDISNSTE 1162
Qy 550 AGOKLFNMLRLKSEDPWTLALENVGAKMNVRLPLNYFEPLFTWLKDKNK--NSFVGV- 606
Db 1163 AGOKLFNMLRLKSEDPWTLALENVGAKMNVRLPLNYFEPLFTWLKDKNK--NSFVGV- 1222
Qy 607 STDWSPVADOS 617
Db 1223 QYNWNTNSARS 1233

RESULT 3
ACET_MOUSE
ID ACET_MOUSE STANDARD; PRT; 732 AA.
AC P22967;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Angiotensin-converting enzyme, testis-specific isoform precursor
DE (EC 3.4.15.1) (ACE-T) (Dipeptidyl carboxypeptidase I) (Kinase II).
GN ACE OR DCP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90318396; PubMed=2164636;
RA Howard T.E., Shai S.-Y., Langford K.G., Martin B.M., Bernstein K.E.;
RT "Transcription of testicular angiotensin-converting enzyme (ACE) is
RL initiated within the 12th intron of the somatic ACE gene.";
RL Mol. Cell. Biol. 10:4294-4302(1990).
CC -1- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
CC THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE
CC VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CC -1- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC oligopeptide|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
CC Asp nor Glu. Converts angiotensin I to angiotensin II.
CC -1- COFACTOR: Binds 1 zinc ion (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Testis-specific;
CC IsoId=P22967-1; Sequence=Displayed;
CC Name=Somatic;
CC IsoId=P09470-1; Sequence=External;
CC -1- TISSUE SPECIFICITY: SPERMATOCYTES, ADULT TESTIS.
CC -1- INDUCTION: EXPRESSION IS THOUGHT TO BE SUBJECT TO HORMONAL
CC REGULATION BY ANDROGENS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M55333; AAA37149.1; -
CC EMBL; M61094; AAA37150.1; -
CC FIR; A35655; A35655.
CC MEROPS; M02.004; -.
DR MGD; MGI:87874; Ace.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Zn_Mtpetpds.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPTIDASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
KW Glycoprotein; Transmembrane; Testis; Signal; Alternative splicing.
FT SIGNAL 1 31
FT CHAIN 32 732
FT DOMAIN 32 684
FT TRANSMEM 685 701
FT DOMAIN 702 732
FT METAL 413 413
FT ACT_SITE 414 414
FT METAL 417 417
FT METAL 441 441
FT DISULFID 182 188
FT DISULFID 382 400
FT DISULFID 568 580
FT CARBOHYD 102 102
FT CARBOHYD 120 120
FT CARBOHYD 139 139
FT CARBOHYD 185 185
FT CARBOHYD 367 367
FT CARBOHYD 616 616
FT SEQUENCE 732 AA; 84047 MW; 16C817E7FBD09BD9 CRC64;
SQ
Query Match 31.1%; Score 1334; DB 1; Length 732;
Best Local Similarity 42.6%; Pred. No. 4.3e-86;
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

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Qy 20 TIEQAKTFLDKFNHEADLFYQSSLASWNTNTTEENVONMNAAGDKVSAFLKEOSTL 79
Db 69 TDEAKADRFVEYDRTAQVLLNEAYEANWQNTNTTIEGSKILLKSTVSNHTLYKGT 128
Qy 80 AQWYPLQIQLNLTVKLQALQONGSSVLSEDKSKRLNTLNTMTSTIYSGKVCNPDNPQ 139
Db 129 AKTFDVSFNQSSIKRIKILQNLDRVLPPELEYNQILLDMETTSYLSNICYTNG-- 186
Qy 140 ECLLEPGLNEAMNSLDYNERLWAWSRSEVSKQRLPYEEVVLKNEAMAHVEDY 199
Db 187 TCMLEPDLTNMATSRYKIELLWAWSRDKVGRALPFPFKYVEFSNKIAKLNGTDA 246
Qy 200 GYWRGDYEVNGVDGYDSRGQIEDVEHTPEEKPLYEHLHAYVRAKLMNAYS-YISP 258
Db 247 GDSWRSLYESDNL-----QDLEKLYOELQPLVNLHAYVRSRHRHYSYINL 296
Qy 259 IGCLPAHLGLGMDGWFNLYSLVFPQKPNIDVTAMDVDQAWDAQRIKFEKPFVSV 318
Db 297 DGFIPAHLLGNNAWQTSNIYDLVVPFAPSMDTTEAMLKQGTWTRMFKEADNFTSL 356
Qy 319 GLPNNTOGFWNSMLTDFGNVQKAVCHPTAWDLGK-DFRILMCTVMTWDDPFLTAHEMG 377
Db 357 GLLPVPPFPFNKSMLEKETDGREVVCCASAWDFYNGKDFRIKQCTSVNMEDLVIAHEMG 416
Qy 378 HIOYDWAYAAQFLLRNGANEGFHEAVGEIMSLSAATPKHLKSLGLSPDFQEDNETEIN 437
Db 417 HIOYFMQYKDLPTVFREGANFGFHEAIGDIMALSVSTPKHLKSLGLSPDFQEDNETEIN 475

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QY 498 CDPASLFHVSNDYSFIRYTRTYQFOFQOEALCOAAKHGPHLKHCDISNSTRAGOKLFNM 557  
DB 1116 FDPCKHVPANVPYRVFVSFIQFOFHEALCRAAGTGLPKCDIYQSKAGKLIADA 1175  
QY 558 LRLKSPPTLALENVVGAKNMVRPLNLYPEELFTWLKQDNK--NSFVGM--STDWSP 612  
DB 1176 MKLGYSKPWPAMKLIITGQPNNSASAMNYPFKPLTEWLVTEENRRHGETLWGPYVWAP 1233  
RESULT 5  
ACE\_CHICK STANDARD; PRT; 1193 AA.  
ID ACE\_CHICK Q10751;  
AC 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Angiotensin-converting enzyme (EC 3.4.15.1) (Dipeptidyl  
carboxypeptidase I) (Kininase II) (Fragment).  
GN ACE OR DCPI  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=95110342; PubMed=7811282;  
RA Esther C.R., Thomas K.E., Bernstein K.E.;  
RT "Chicken lacks the testis specific isozyme of angiotensin converting  
enzyme found in mammals."  
RL Biochem. Biophys. Res. Commun. 205:1916-1921(1994).  
CC THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF  
VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN  
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide  
oligopeptide--|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither  
Asp nor Glu. Converts angiotensin I to angiotensin II.  
CC -!- COFACTOR: Binds 2 zinc ions (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL; L40175; AAA75554.1; -;  
CC PIR; JC2489; JC2489.  
CC MEROPS; M02.001; -;  
CC InterPro; IPR001548; Peptidase M2.  
CC InterPro; IPR006025; Zn\_MTPeptide.  
CC Pfam; PF01401; Peptidase M2; 2.  
CC PRINTS; PR00791; PEPDIP7ASEA.  
CC ProDom; PD004184; Peptidase M2; 2.  
CC PROSITE; PS00142; ZINC\_PROTEASE; 2.  
CC K0W Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;  
KW Glycoprotein; Transmembrane; Repeat.  
FT NON\_TER 1 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN <1 1156 POTENTIAL.  
FT TRANSMEM 1157 1173 POTENTIAL.  
FT DOMAIN 1174 1193 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 125 481  
FT REPEAT 723 1079  
FT METAL 288 288  
FT ACT\_SITE 289 289  
FT METAL 292 292  
FT METAL 866 866  
FT ACT\_SITE 887 887  
ZINC 1 (CATALYTIC) (BY SIMILARITY).  
ZINC 1 (BY SIMILARITY).  
ZINC 1 (CATALYTIC) (BY SIMILARITY).  
ZINC 2 (CATALYTIC) (BY SIMILARITY).  
ZINC 2 (BY SIMILARITY).

FT METAL 890 890 ZINC 2 (CATALYTIC) (BY SIMILARITY).  
FT CARBOHYD 11 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 60 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 216 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 407 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 447 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 485 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 513 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 555 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 575 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 658 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1089 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1193 AA; 137820 MW; 954472A18EA471C7 CRC64;  
Query Match 30.6%; Score 1312; DB 1; Length 1193;  
Best Local Similarity 40.4%; Pred. No. 3.1e-84;  
Matches 264; Conservative 110; Mismatches 243; Indels 36; Gaps 10;  
QY 22 BEQAKTFDLKFNHEADLFPYQSSLASWNYNTNITENVQNNMAGDKWSAFLEKQSTLAAQ 81  
DB 544 EAQAKFEFLSEYNSTAEVVMNAYTEASWEYNTNITDHNKEVLMLEKRLAWSKHTIEYGMAR 603  
QY 82 MYPLOEIQNLTVKLOLQALQQNGSSVLSEDKSKRLNTILNTMTSTIYSTGKVCNPDN--P 138  
DB 604 QFDPSPQDETTRINKLSVLERAALPEDELKEYNTLLSDMETTYSVAKVCRENNTFHP 663  
QY 139 QECILLEPGINIMANSLDYNERLMAWSRSEVKQLRPLYEYVVLKNEVARAHYED 198  
DB 664 -----LDPDLTDLATSRDYNELLFAWKGNWDASAKIKDKYKRYVELSNKAALVNGYD 718  
QY 199 YGDYWGEGVNGVGDYDSRQQLTEVDHTEETKPLEYHHLHAYVRAKLNNAY--PSYIS 257  
DB 719 NGAYWASLLETPTFE-----EDLELYLQQLYPLNLHAYVRRALYKNGYAEHIS 768  
QY 258 PIGCLPAHLGLDMGWRFTNLSLTVFPFGQKNIDVTDAMVDQAWDAQRIKFAEAEKFFVS 317  
DB 769 LKGPIDPAHLGLNMAQWSNIFDLVMPFPDATKVDATPAMKQGWTPKXMFESDRFFTS 828  
QY 318 VGLPNTQGFWSMLTDPQNVKQVCHPTAMD--GKGFRIIMCTKVTMDDFLTAHHEM 376  
DB 829 LGLIPMPQBFWDKSMTEKPADGREVVCHASANDFYNRKDFRIKQCTVVMDDLLITVHEM 888  
QY 377 GHIQYDMAYAAQPFLLRNGANEGFHAIVEIMSLSAATPKHLKSGILLSPDQEDNETEI 436  
DB 889 GHVQYFLQYMDQPISPFDGANPGFHAIGDVMVALSVSTPKHLHSINLLD--QVTNEESDI 947  
QY 437 NFKLKQALITVGTLPFTYMLEKRWVVFGEIPKQDMKMKWEMKREIVGVVPEVPHDET 496  
DB 948 NYLMSIALDKIAELFPFGYLMQWRKVFDRKEDYEQWNLRLKYQGLCPPVERSED 1007  
QY 497 YCDPASLFHVSNDYSFIRYTRTYQFOFQOEALCOAAKHGPHLKHCDISNSTRAGOKLFN 556  
DB 1008 DFDPGAKFHIPANVPYRVFVSFIQFOFHEALCRAAGTGLPKCDIYQSKAGKLIADA 1067  
QY 557 MLRLKSPPTLALENVVGAKNMVRPLNLYPEELFTWL--KDNKNSFVGM--STDWSPY 613  
DB 1068 AMKLGSKPWPPEAMKLIITGQPNNSAALMSYFPEPLMTLVKRNTEGVLWGPYVWAP 1127  
QY 614 ADQSIKVRISLKSALG-----DKAYEMNDNEMYLFRSSVAYAMQYFLKVK 659  
DB 1128 AVTEFFHAATDTADFLGNSVGTQKATAGAW-----VLLALAVELITSIFLGVK 1175  
RESULT 6  
ACE\_RAT  
ID ACE\_RAT PRT; 1313 AA.  
AC P47820;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)  
DE (ACE) (Dipeptidyl carboxypeptidase I) (Kininase II).  
GN ACE OR DCPI.

OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
[1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=94121659; PubMed=8292044;  
RA Koike G., Krieger J.E., Jacob H.J., Mukoyama M., Pratt R.E.,  
R Dzuu V.J.;  
RT "Angiotensin converting enzyme and genetic hypertension: cloning of  
RT rat cDNAs and characterization of the enzyme";  
RL Biochem. Biophys. Res. Commun. 198;380-386(1994).  
[2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=Lewis/N; TISSUE=Lung;  
RA Jafarian-Tehrani M., Listwak S., Barrientos R.M., Michaud A.,  
RA Corvol P., Sternberg E.M.;  
RT "Characterization of a missense mutation in the angiotensin  
RT I-converting enzyme cDNA in exudative inflammation resistant F344/N  
RT rats.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF  
CC THE TERMINAL HIS-LEU. THIS RESULTS IN AN INCREASE OF THE  
CC VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.  
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,  
CC oligopeptide -|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither  
CC Asp nor Glu. Converts angiotensin I to angiotensin II.  
CC -!- COFACTOR: Binds 2 zinc ions (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Somatic;  
CC IsoId=P47820-1; Sequence=Displayed;  
CC Name=Testis-specific;  
CC IsoId=P47820-2; Sequence=Not described;  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.  
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DR EMBL; U03708; AAA82110.1; -;  
DR EMBL; U03734; AAA82111.1; -;  
DR EMBL; AF201332; NAG35597.1; -;  
DR PIR; JC2038; JC2038.  
DR MEROPS; M02.001; -;  
DR InterPro; IPR001548; Peptidase M2.  
DR InterPro; IPR006025; Zn\_Mtpeptidse.  
DR Pfam; PF01401; Peptidase M2; 2.  
DR PRINTS; PR00791; PEPTIDTASEA.  
DR PRODOM; PD004184; Peptidase M2; 2.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 2.  
DR KX Hydroxylase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;  
KW Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing.  
FT SIGNAL 1 35  
FT CHAIN 36 1313  
FT ISOFORM  
FT DOMAIN 36 1265  
FT TRANSMEM 1266 1282  
FT DOMAIN 1283 1313  
FT REPEAT 233 589  
FT REPEAT 831 1187  
FT METAL 396 396  
FT ACT\_SITE 397 397  
FT METAL 400 400  
FT METAL 994 994  
FT ACT\_SITE 995 995

FT METAL 998 998  
FT CARBOHYD 44 44  
FT CARBOHYD 60 60  
FT CARBOHYD 80 80  
FT CARBOHYD 117 117  
FT CARBOHYD 152 152  
FT CARBOHYD 166 166  
FT CARBOHYD 224 224  
FT CARBOHYD 515 515  
FT CARBOHYD 683 683  
FT CARBOHYD 701 701  
FT CARBOHYD 720 720  
FT CARBOHYD 766 766  
FT CARBOHYD 948 948  
FT CARBOHYD 1197 1197  
FT VARIANT 207 207  
SQ SEQUENCE 1313 AA; 150907 MW; 8C85D0015F129591 CRC64;  
  
Query Match 30.5%; Score 1310; DB 1; Length 1313;  
Best Local Similarity 42.0%; Pred. No. 4.8e-84;  
Matches 251; Conservative 115; Mismatches 214; Indels 18; Gaps 7;  
  
QY 20 TIEQAKTFLDKFNEAEDLFYQSSLASWNTNITEVQNMNAGDKWSAFLKEQSTL 79  
DB 650 TDEAKANFVEYDRTAKLVNWEYAEANWHYNTITTEGSKLLQKKEVSNHLKYGTW 709  
QY 80 AQMPYLPQRIQNLTKVLQALQALQONGSSVLSDEKSKRLNTILNTMTSTIYSGKVCNPNPQ 139  
DB 710 AKTFDVSFNQSTIKRIIKKQNVDRVLPPELLEYNQIILDMETTSVANVCVTNG-- 767  
QY 140 ECLLEPGELNEIMANSLDYNERLWAWESRSEVGKQLRPLYEEVVLNENARAHNEDY 199  
DB 768 TCLSLEPDLTNMATSRKYEBELLWYKSWRDKVGRALFFPFKYVDFSNKIAKLNGYSDA 827  
QY 200 GDYMRGDYEVNGVGDYDSRGQIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258  
DB 828 GDSWSSYESSDLE-----QDLEKLYQELQPLVNLHAYVRRSLHRHGYSEYNL 877  
QY 259 IGLFAHLGDMGWGFTNLSLTVPFQKQKNDVTDAMVDQANDQAIKFAEKFFVSV 318  
DB 878 DGPFAHLGLGNWAGTWSNIYDLVAPFSPASISIDATEAMIKQGTTPRIFKEADNFFTSL 937  
QY 319 GLPNTQGFWNSMLTDGNGQKAVCHPTAMDGKG-DFRILMCTKVMTDDFLTAHBMG 377  
DB 938 GLLPVPFPFWKSMLEKTDGSEVVCASANDFYNGKDFRIKQCTSVNWEELVIAHBMG 997  
QY 378 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSGLLSPDQEDNETIN 437  
DB 998 HIQYPMQYKDLPTVTEGANGPGHEAIGDVLALSYSTPKHLHLLLSSE-GSGYEHDIN 1056  
QY 438 FLLKQALTIQGLTPETYMLEKRWNVFKEIPEKQOMKMKWEMKREIVGVVPEVPDDET 497  
DB 1057 FLMKWALDKIAFIPFSLIDQWRVFGSITKENYNGEWSLRKLYQGLCPVPRSQGD 1116  
QY 498 CDPASLFHVSNDYSFIRYTRTYQFQCEALCOAAKHEGPHLHKCDINSTNTEAGOKLFNM 557  
DB 1117 FDPGSKFHPANVPVIRYFISFIIQFQHEALCRAAGHTGPLYKCDIYQSKAEAGLLADA 1176  
QY 558 LELGKSEPTWALENVGAKNVAEPLNLYPEPLFTWLKDQNK--NSFVGM-STOWSP 612  
DB 1177 MKLGYSQKQFPAWKIITGQPNMSASAINMYFAPLTELVTENRRHGHETGLGWPEYTWTP 1234  
  
RESULT 7  
ACE\_RABIT  
ID ACE\_RABIT STANDARD; PRT; 1310 AA.  
AC P12822; 002852;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)  
DE (ACE) (Dipeptidyl carboxypeptidase I) (kininase II).  
GN ACE OR DCPI.

OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RC TISSUE=Liver;  
 RX MEDLINE=92179960; PubMed=1311831;  
 RA Thekkumkara T.J., Livingston W. III, Kumar R.S., Sen G.C.;  
 RT "Use of alternative polyadenylation sites for tissue-specific  
 transcription of two angiotensin-converting enzyme mRNAs";  
 RL Nucleic Acids Res. 20:683-687(1992).  
 RN [2]  
 RN REVISIONS.  
 RP Sen G.C.;  
 RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE OF 1-88 FROM N.A.  
 RP TISSUE=Liver;  
 RX MEDLINE=91139683; PubMed=1847388;  
 RA Kumar R.S., Thekkumkara T.J., Sen G.C.;  
 RT "The mRNAs encoding the two angiotensin-converting isozymes are  
 transcribed from the same gene by a tissue-specific choice of  
 alternative transcription initiation sites";  
 RL J. Biol. Chem. 266:3854-3862(1991).  
 RN [4]  
 RN SEQUENCE OF 34-55.  
 RP TISSUE=Lung;  
 RX MEDLINE=84051289; PubMed=6314908;  
 RA Iwata K., Blacher R., Soffer R.L., Lai C.Y.;  
 RT "Rabbit pulmonary angiotensin-converting enzyme: the NH2-terminal  
 fragment with enzymatic activity and its formation from the native  
 enzyme by NH4OH treatment";  
 RL Arch. Biochem. Biophys. 227:188-201(1983).  
 CC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF  
 THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE  
 VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.  
 CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,  
 oligopeptide-I-Xaa-Xbb, when Xaa is not pro, and Xbb is neither  
 Asp nor Glu. Converts angiotensin I to angiotensin II.  
 CC -!- COFACTOR: Binds 2 zinc ions (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Somatic;  
 CC IsoId=PI2822-1; Sequence=Displayed;  
 CC Name=Testis-specific;  
 CC IsoId=P22968-1; Sequence=External;  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X62551; CAA44428.1; --  
 DR EMBL; M58579; AAA31151.1; ALT\_SEQ.  
 DR PIR; S35484; S35484.  
 DR MEROPS; M02.003; --  
 DR InterPro; IPR001548; Peptidase\_M2.  
 DR InterPro; IPR006025; Zn\_Mtpeptidse.  
 DR Pfam; PF01401; Peptidase\_M2; 2.  
 DR PRINTS; PR00791; Peptidase\_M2.  
 DR PRODOM; PD004184; Peptidase\_M2; 2.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 2.  
 KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;  
 FT Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing.  
 FT SIGNAL 1 33  
 FT CHAIN 34 1310 ANGIOTENSIN-CONVERTING ENZYME, SOMATIC

FT DOMAIN 34 1263  
 FT TRANSMEM 1264 1380  
 FT DOMAIN 1281 1310  
 FT REPEAT 232 588  
 FT REPEAT 829 1185  
 FT METAL 395 395  
 FT ACT\_SITE 396 396  
 FT METAL 399 399  
 FT METAL 992 992  
 FT ACT\_SITE 993 993  
 FT METAL 996 996  
 FT CARBOHYD 59 59  
 FT CARBOHYD 79 79  
 FT CARBOHYD 151 151  
 FT CARBOHYD 323 323  
 FT CARBOHYD 449 449  
 FT CARBOHYD 513 513  
 FT CARBOHYD 681 681  
 FT CARBOHYD 699 699  
 FT CARBOHYD 718 718  
 FT CARBOHYD 946 946  
 FT CARBOHYD 1195 1195  
 FT CONFLICT 48 48  
 SQ SEQUENCE 1310 AA; 150405 MW; 04777FAB17981DEA CRC64;  
 Query Match 29.9%; Score 1283.5; DB 1; Length 1310;  
 Best Local Similarity 36.8%; Pred. No. 3.5e-82;  
 Matches 275; Conservative 135; Mismatches 262; Indels 75; Gaps 17;  
 Qy 7 LLSLVAVTAAGSTI-----EQAKTFDKFNHEADLFYQSSLASWYNTNI 54  
 Db LLLLLPPPAALTLDPLGDFADAEAGARLFASSYSSAEQVLFRTSTAASWAHDTNI 80  
 Qy 55 TEENVQNMNAGDKWSAFLEKEOSTLAQMYPOE1-----QNLTKLQALQONGSS 106  
 Db TANARQEB-----EALLSQFAEWKAKELYPWQNTDPELRRIIGAVRTLGA 135  
 Qy 107 VLSEKSKRLNTILNTMTSTIYTGKVCNPDNPQECLELLPEGLNEIMANSLDNERLWAE 166  
 Db NLPLAKRQQVNSLLSNMSQIYSTGKVCNPKTASCWSLDPDLNIIASSRSYAMLLFAWE 195  
 Qy 167 SWRSEVKGQLRPLYEEVVLKEMARANYEDYDWRGDYGVNGVDYDSRGQIIEV 226  
 Db GHNNAVGIPLKPLYQEFALSNAYQDGFSDTGAYRWSYDSPTPE-----EDL 245  
 Qy 227 EHTPEEIKPLYEHLHAYVRRAKLMNAY-PSYISPGICLPAHLGDMGFRWTNLSYTVDF 285  
 Db ERIYHQLPLEPLYNLHAYVRRVLRHRYGDRYINLRGPIPAHLGNMWAQSWESIYDMVVPF 305  
 Qy 286 GQKPNIDVTAMVDQAWDAQRIFKEAEKFPVSGLPNMTGQFWNSMLTDPGVQKAVCH 345  
 Db PDKPNLDVTSTMVQKGNATHMPFVAEEFTSLGLLPMPPEFWAESMLEKPEGREVVCH 365  
 Qy 346 PTAWDL-GKGDFTLMCTKVTMDDFLTAFHEMIGHIYQDMAYAAQPFLLRNGANEGHEAV 404  
 Db ASAWDFYNRKDFRIKQCTQVTMBQLSVHEHMGHVQYLYQYKQDPVSLRR-ANPGFHEAI 424  
 Qy 405 GEINSLSAAPKHLKSLGILLSPQEDNETEINFLIKQALTIVGLTLPFTVMLEKRWVWF 464  
 Db GDVLALSVSPTFAHLKTKGLLD-HVTNDESDINYLKMALEKTAFLPFGVLQVQWGVF 483  
 Qy 465 KGEIPKQWKKWEMEREIVGVVEVPVPHDETCDPASLPHVSNDSYFIRYTRTYQFQ 524  
 Db SGRTFSSRYNFDWYLLTKYGCICPPVVRNETHFDAGAKPHIPSVTPYIRYFVSVLQFQ 543  
 Qy 525 PQEALCOAAKHGELPHKCDI-SNSTEAGOKLFNMLRLGKSEPTWALLENVVGAKMNVRL 584  
 Db FHOALCMAGHQGELPHQCDIYQSTRAGAKLRAVLQAGCSRPOEVLKQMWVASDALQPL 603  
 Qy 585 LNYPELFTMLKQONKNS--FVGW-STDWSPYADQSIKVAISLSKALG-----DKA 632  
 Db LDYFPQVTLQEQNERNGEVLGHPEYQWEPPLPNNYPEGIDLVTDAAEASRFVEEYDRS 663

QY 633 YE-WND-----NEMYLFRSVAYAMQVFLKVKQNMILFGEDVVRVANLKRISFNPF 684  
 DB 664 FQAVNVEAYEANNYNNTITTEASKILLQKNMOIANHTLYG-----NWARFVDVSNF 716  
 QY 685 VTAP-----KNVSD-----IIPRTVEK 702  
 DB 717 QNATSKRIIKVQDLQRAVLVPELES 743

RESULT 8  
 ACET RABBIT  
 ID ACET RABBIT STANDARD; PRT; 737 AA.  
 AC P22968;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Angiotensin-converting enzyme, testis-specific isoform precursor  
 DE (EC 3.4.15.1) (ACE-T) (Dipeptidyl carboxypeptidase I) (Kinase II).  
 AC ACET RABBIT.  
 OS Oryctolagus cuniculus (Rabbit).  
 GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=New Zealand white; TISSUE=Testis;  
 RX MEDLINE=89380303; PubMed=250457;  
 RA Kumar R.S., Kusari J., Roy S.N., Soffer R.L., Sen G.C.;  
 RT "Structure of testicular angiotensin-converting enzyme. A segmental  
 RT mosaic isoform.";  
 RL J. Biol. Chem. 264:16754-16758 (1989).  
 RN [2]  
 RP SEQUENCE OF 1-117 FROM N.A.  
 RX MEDLINE=91139683; PubMed=1847388;  
 RA Kumar R.S., Thekkumkara T.J., Sen G.C.;  
 RT "The mRNAs encoding the two angiotensin-converting isozymes are  
 RT transcribed from the same gene by a tissue-specific choice of  
 RT alternative transcription initiation sites.";  
 RL J. Biol. Chem. 266:3854-3862 (1991).  
 GC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF  
 CC THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE  
 CC VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.  
 CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,  
 CC oligopeptide.-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither  
 CC Asp nor Glu. Converts angiotensin I to angiotensin II.  
 CC -!- COFACTOR: Binds 1 zinc ion (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Testis-specific;  
 CC IsoId=P22968-1; Sequence=Displayed;  
 CC Name=Somatic;  
 CC IsoId=P12822-1; Sequence=External;  
 CC -!- TISSUE SPECIFICITY: SPERMATOCTYES, ADULT TESTIS.  
 CC -!- INDUCTION: EXPRESSION IS THOUGHT TO BE SUBJECT TO HORMONAL  
 CC REGULATION BY ANDROGENS.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.  
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 CC  
 CC -----  
 CC EMBL; J05041; AAA31153.1; -;  
 CC EMBL; M58580; AAA31152.1; -;  
 CC PIR; A34402; A34402.  
 CC MEROPS; M02.004; -;  
 CC InterPro; IPR001548; Peptidase M2.  
 CC InterPro; IPR006025; Zn\_MTPeptide.

PFam; PF01401; Peptidase M2; 1.  
 DR PRINTS; PRO0791; PEPTIDASEA.  
 DR PRODom; PDC04184; Peptidase M2; 1.  
 DR PROSITE; PS00142; ZINC PROTEASE; 1.  
 KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;  
 KW Glycoprotein; Transmembrane; Testis; Signal; Alternative splicing.  
 FT SIGNAL 1 32  
 FT CHAIN 33 737 ANGIOTENSIN-CONVERTING ENZYME, TESTIS-  
 FT SPECIFIC ISOFORM.  
 FT DOMAIN 33 690 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 691 707 POTENTIAL.  
 FT DOMAIN 708 737 CYTOPLASMIC (POTENTIAL).  
 FT METAL 419 419 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 420 420 BY SIMILARITY.  
 FT METAL 423 423 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 447 447 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT DISULFID 188 194 BY SIMILARITY.  
 FT DISULFID 388 406 BY SIMILARITY.  
 FT DISULFID 574 586 BY SIMILARITY.  
 FT CARBOHYD 108 108 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 373 373 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 737 AA; 83923 MW; FC43CCT76655C3DCA CRC64;  
 Query Match 29.9%; Score 1283; DB 1; Length 737;  
 Best Local Similarity 40.8%; Pred. No. 1.7e-82;  
 Matches 250; Conservative 112; Mismatches 213; Indels 38; Gaps 10;  
 QY 20 TIEQAKTFDKEFHEAEADLFYQSSLASWNYNTNITEB-----NVQNMN--AGDKW 69  
 DB 75 TDEASRFVEEYDRSFQAVNVEAYEANNYNNTITEASKILLQKNMOIANHTLYG 134  
 QY 70 SAFLKEOSTLAQMYPLQEIQLNFKVLQALQNGSSVLSEDSKXRLNTILNTMTTIST 129  
 DB 135 -----ARRFDVSNFQATSKRIKKVDQRAVLVPELESYQILDMETIYSV 184  
 QY 130 GKVCNPDNPQECILLPEGLNEIMANSLDYNERLWAMESWRSEVGKGLRLPYEYVLKNE 189  
 DB 185 ANVCRVDG--SCQLPEFLTNLMTATSKYDELLWWTSDKVGRAILPYFXYVEFIN 242  
 QY 190 MARANHYEDYGVWGDYEVNGVDYSGRLIEDVHTFEIKPLYEHLHAYVRAKLM 249  
 DB 243 AARLNGYVDAGDSWRSMYETPTLE-----QDLERLFOELQPLYNLHAYYGRALH 292  
 QY 250 NAY-PSYISIGCLPAHLGDMWGRFTNLYSLTVPFGQKPNIDVTDAVDAQDAQRI 308  
 DB 293 RHYGAQHINLEGPIPAHLGDMWGRFTNLYSLTVPFGQKPNIDVTDAVDAQDAQRI 352  
 QY 309 KEAEKFFVSGLPNMTQGFWENSLTDPGNVQKAVCHPTAWDLGKG-DPRILMCTKV 367  
 DB 353 EADKFFISLGLLPVPEPFWKNMSEKPTDGEVWCHASAWDFYQKOPRIKQCTV 412  
 QY 368 DFLTAHEMGHIQYDMAYAAQPTLLRNGANEGPHEAVGEIMSLSAATPKHLSIG 427  
 DB 413 DLVVVHEMGHIQYFMOYKDLPLVALREGANPGPHEAIGDVLALSYSTPKHLSIN 472  
 QY 428 PQENETETNPLKQALITVGTLPFTYMLEKRWVFKGEIPDQMKKQWMEKEIVGV 487  
 DB 473 -GGGYEHINFLMKMALDKIAFPFSYLVDEWRWRVFDGSIITKENYNQEWWSRLKY 531  
 QY 488 VEPVPHDTCDPASLPHVSNDSFYRYTTRTYLQFQFQFQFQFQFQFQFQFQFQF 547  
 DB 532 CPPAPRSQGDFFGAKFHIPSSVPYRYRVSVFTIQFQFHEALCKAAGHTGLHTCD 591  
 QY 548 TERQCKLFNMLRKGKSPWTLALENVVGAKNMVRPLNYPFLPFWLQDN--KNSFVG 605  
 DB 592 KEAGKRLADAMKLGYSKGPWEAKMKVITGPNNNSASAMNYPKPLMDWLLTENG 651  
 QY 606 W-STDWSPYADQS 617  
 DB 652 WQYTWTPNSARS 664

[illegible]



DE DE Angiotensin-converting enzyme precursor (EC 3.4.15.1) (Dipeptidyl  
GN carboxypeptidase I) (Kininase II).  
ACB.  
OS Haematobia irritans exigua (Buffalo fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;  
OC Muscidae; Haematobia.  
OX NCBI\_TaxID=34678;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96215437; PubMed=8647080;  
RA Wiffels G.L.; Fitzgerald C., Gough J., Riding G.A., Elvin C.,  
RT Kemp D.J., Willadsen P.;  
RL "Cloning and characterisation of angiotensin-converting enzyme from  
the dipteran species, Haematobia irritans exigua, and its expression  
in the maturing male reproductive system.";  
CC Eur. J. Biochem. 237:414-423(1996).  
CC -!- FUNCTION: INVOLVED IN THE SPECIFIC MATURATION OR DEGRADATION OF A  
CC NUMBER OF BIOACTIVE PEPTIDES.  
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,  
CC oligopeptide [-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither  
CC Asp nor Glu. Converts angiotensin I to angiotensin II.  
CC -!- COFACTOR: Binds 1 zinc ion (By similarity).  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE COMPOUND GANGLION AND IN THE  
CC POSTERIOR REGION OF THE MIDGUT.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.  
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CC -----  
DR EMBL; L43965; AAA70427.1; -  
DR PIR; S65472; S65472.  
DR MEPROPS; M02.003; -  
DR InterPro; IPR001548; Peptidase M2.  
DR InterPro; IPR006025; Zn\_MTPeptidse.  
DR Pfam; PF01401; Peptidase M2\_1.  
DR PRINTS; PR00791; PEPDIPFASAA.  
DR PRODOM; PD004184; Peptidase M2; 1.  
DR PROSITE; PS00142; ZINC PROTEASE; 1.  
DR Hydroxylase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;  
KW Glycoprotein; signal.  
FT SIGNAL 1 FT POTENTIAL.  
FT CHAIN 18 611 ANGIOTENSIN-CONVERTING ENZYME.  
FT METAL 367 367 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 368 368 BY SIMILARITY.  
FT METAL 371 371 ZINC (CATALYTIC) (BY SIMILARITY).  
FT CARBOHYD 53 53 N-LINKED (GLCNAC.. ) (POTENTIAL).  
FT CARBOHYD 196 196 N-LINKED (GLCNAC.. ) (POTENTIAL).  
FT CARBOHYD 531 531 N-LINKED (GLCNAC.. ) (POTENTIAL).  
SQ SEQUENCE 611 AA; A43D6DF5A83ECB53 CRC64;  
  
Query Match 24.7%; Score 1058; DB 1; Length 611;  
Best Local Similarity 37.2%; Pred No. 8, 7e-67;  
Matches 223; Conservative 108; Mismatches 246; Indels 22; Gaps 7;  
  
QY 8 LLSLVAVTAQAQTSTBEQAQTFIDKFNHREAEFLFYQSSLAGSNWNTNITEENVOMNAGD 67  
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||:  
QY 8 ILAGLAVCGHATKEEIVATEYLQNTLNKLAKHTVETSVSWAYASNITDENELRNEISA 67  
DB :|::||::||::||::||::||::||::||::||::||::||::||::||:  
QY 68 KWSAFLEKQSTLAQMYPLOEQIQLTVKLQALQONGSSVLSEDKSKRLNTILNTMSTTY 127  
DB :|::||::||::||::||::||::||::||::||::||::||::||::||:  
QY 68 ENAKFLKEVAKOIQENRWNYTGSDVRRPFKSLKTGYSALEPAEDYAELEVLVSAMESNF 127  
DB :|::||::||::||::||::||::||::||::||::||::||::||::||:  
QY 128 STGVKNPNDFQC-LLLEPLGLNEIMANSLDYNRELRAWESWTSEVKQLRPLYEYVVL 186  
DB :|::||::||::||::||::||::||::||::||::||::||::||::||:  
QY 128 AKRVCDCKYNSAKCDLSDPEEEIITIKSRDPSELKYTWTFQDYDKAGTPTRSNFKVEL 187  
DB :|::||::||::||::||::||::||::||::||::||::||::||::||:  
QY 187 KNEMAZANHVEDYGDWRGDVEWGVDGYDSRQLIED-VHETFFEIKPLVEHLHAYVR 245

RESULT 10	STANDARD;	PRT;	611 AA.
ACE HAEIE			
ID ACE HAEIE			
AC Q10715;			
DT 01-NOV-1997	(Rel. 35, Created)		
DT 01-NOV-1997	(Rel. 35, Last sequence update)		
DT 28-FEB-2003	(Rel. 41, Last annotation update)		



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Db 188 NTKSALNNTDGAELVWDEYE-----DATFEOZLAIFAIEDIKPLVDQVHGVR 236
Qy 246 AKLWVAY-PSYISPGICLPAHLIGDWGFWNTNLSYLVTPFOCKNNIDVTDAMVDQAWDA 304
Db 237 YRLNKFVGDVEVSKTGLPMLHGNWAOQWSIADIVSPFPEKPLVDVSDBMVAQGYTP 296
Qy 305 QRIFKEAEKFFSVSGVFNMTQGFWNSMLTDPGNOKAVCHPTAWDLG-KGDFRILMCTK 363
Db 297 LKMFQMGDDFFQSNGLKCLQFQFWKSIKPKDDGRDLVCHASANDFYLTDDVRIKQCTR 356
Qy 364 VTWDDFLTAHENGHIQDYWAYAOPFLRNGANGEGFHEAVGEIMSLNATPKHLKSIGL 423
Db 357 VTQQPFVHENGHIQFYQYQHPVYRTGANGPFGFHEAVGDVLSVSTPKHLERVGL 416
Qy 424 LSPDFQEDNETENFLKQALTYGLTFPTMLKRWNVFVKEGEPKQOMKMKWEMKRE 483
Db 417 LK-NYVSDNEARINQLFLTLALDKIVLPFAFTMDKYRWALFRGQADKSEWNCAPWKLEE 475
Qy 484 IGVVPEVPHEDEYCDPASLFPHVSNDSYSTRYVTRLYQFQEQALCQAA-----KHGG 537
Db 476 YSGIEPPVTEKDFDAPAKYHVSADVLYRVLVSFIIOQPKSACITAGSYVNPQTEY 535
Qy 538 PLKXCDISNSTEAGQKLFNMLRLKSEPTWTLALENVVGAKNMVRPLNLYEPELFTWLK 596
Db 536 PLONCDIYGSKEAGKLFENMLSLGASKPWPDALEAFNGERTWTGKAIEAYEPELVRWLE 594

RESULT 11
YPWA_BACSU
ID YPWA_BACSU STANDARD; PRT; 501 AA.
AC P50848;
JT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical metalloprotease ypwA (EC 3.4.24.-).
GN YPWA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
[1]
SEQUENCE FROM N.A.
RC STRAIN=168 / Marburg;
RC MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
RA Serror P.,
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the serA and kgd loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
[2]
SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ocasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bortolero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Broutillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Gollighly B.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haeft J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Icaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Fujic P., Purnelle G., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche S., Rose M., Sadale Y.,

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RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpatra F., Tognoni A.,
RA Tsoato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.P., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (Potential).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M32.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L47838; AAB38482.1; .
DR EMBL; L77246; AAA96610.1; .
DR EMBL; Z91115; CAB14125.1; .
DR PIR; D69943; D69943.
DR MEROPS; M32; UPK; .
DR Subtilisin; BG11458; ypwA.
DR InterPro; IPR001333; Peptidase M32.
DR InterPro; IPR006025; Zn_Mtpeptidse.
DR Pfam; PF02074; Peptidase M32; 1.
DR PRINTS; PR00988; CRBOXYPTASET.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
DR KW Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
KW Complete proteome.
FT METAL 285 285 ZINC (CATALYTIC) (POTENTIAL).
FT ACT_SITE 286 286 POTENTIAL.
FT METAL 269 269 ZINC (CATALYTIC) (POTENTIAL).
SQ SEQUENCE 501 AA; 58174 MW; A7489BAEFA38F82 CRC64;

Query Match 3.1%; Score 135; DB 1; Length 501;
Best Local Similarity 20.9%; Pred. No. 0, 058;
Matches 98; Conservative 65; Mismatches 164; Indels 142; Gaps 26;

Qy 180 YEEYVL--KNEMA--RANHEDYV-----DWRGDEYEVNGVDGYDS 218
Db 103 YXEYVILCSKASTAWEAKGSDSFLSPYLEQIEFNKRFITYW-----GYQ-- 150
Qy 219 RQGLIEDVEHTPEEIKPLYEHLHAYVRAKLMNAYPSVISPTGCLPAHLGLDMNGRFTNL 278
Db 151 -----EHPYDALLDLE--PGVTVKVLD-----QLPAEL 177
Qy 279 YSLTYPF-----CKENIDVTAMVDQAWDAQRIPKAEKFPVSVGLPNMTQGFWNS 331
Db 178 KEAIIPLVKQVTASGNK-----DTSFITKAFPKQKQKLSLYFLOELGYDF---- 224
Qy 332 MLTDPGNQKAVCHPTAWDLGKGFRIIMCTKVTWDDFLTA-----HHEMGHIQYD--MAY 385
Db 225 ---DGRLLDET-VHPFATLNRGDRV--TTRYDEKDFRTAIFGTIECCGHAIVEQWIDE 278
Qy 386 RAQPFLLRNGANGEGHEA-----VGE-----IMLSAATPKHLKSLGSLSPDF- 428
Db 279 ALSGNLSGASMGHSQSFLFYENFGNRKHFVTPYKKIQEASPVQFQKDISL--DDVF 336
Qy 429 QEDNETENFLKQAA--LITVGLTFPTMLKRWNVFVKEGEPKQOMKMKWEMKREIVG 486
Db 337 RAINEKSGSFTRVEADELTYPHLIIIRYIEBK-----AIFSNEVSVEDLPSLWNNQKYQDYL 393
Qy 487 VVEPVPHEDEYCDPASLFPHVSNDSYSTRYVTRLYQFQEQALCQ-----AAKHEGPL 539
Db 394 I---TPQDAEGILODFHWAGDGYFSPFVALGYWAAQLKQKMLDLPDFDALLERGEF 450
Qy 540 HKCDISNSTEAGQKLFNMLRL-GKSEPTWTLALENVVGAKNMVRPLNLY 587

```

Db 451 HPK-----QWTEKHVHGKPKPLDKDQATG-BELNRYLIDY 490

RESULT 12

GLGB BACSU STANDARD; PRT; 627 AA.

CC 01-FEB-1995 (Rel. 31, Created)

CC 01-FEB-1995 (Rel. 31, Last sequence update)

CC 15-SEP-2003 (Rel. 42, Last annotation update)

CC 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching enzyme).

CC GN GLGB.

CC Bacillus subtilis.

CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

CC NCBI TaxID=1423;

CC [1]\_SEQUENCE FROM N.A.

CC STRAIN=168;

CC MEDLINE=94195107; PubMed=8145641;

CC Kiel J.A.K.W., Boels J.M., Beidman G., Venema G.;

CC "Glycogen in Bacillus subtilis: molecular characterization of an

CC operon encoding enzymes involved in glycogen biosynthesis and

CC degradation."

CC Mol. Microbiol. 11:203-218(1994).

CC [2]\_SEQUENCE FROM N.A.

CC STRAIN=168;

CC MEDLINE=98048467; PubMed=9387221;

CC Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;

CC "Sequencing and functional annotation of the Bacillus subtilis genes

CC in the 200 kb rnb-dnaB region."

CC Microbiology 143:3431-3441(1997).

CC [3]\_SEQUENCE FROM N.A.

CC STRAIN=168;

CC MEDLINE=98044033; PubMed=9384377;

CC Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

CC Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

CC Bortiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

CC Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

CC Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

CC Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,

CC Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

CC Fritz S., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

CC Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,

CC Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

CC Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

CC Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

CC Kobayashi Y., Koeter P., Koningsstein G., Krogh S., Kumano M.,

CC Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

CC Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

CC Medina N., Meliado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

CC Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

CC Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

CC Presecan E., Pujic P., Furnelle B., Rapoport R., Rey M., Reynolds S.,

CC Rieger M., Rivolta C., Rochelle E., Roche B., Rose M., Sadaie Y.,

CC Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

CC Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

CC Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

CC Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

CC Totsato V., Uchiyama S., Vandendol M., Vannier P., Vassarotti A.,

CC Viari A., Wambutt R., Wedler H., Wedler H., Weitzenecker T.,

CC Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

CC Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;

CC "The complete genome sequence of the Gram-positive bacterium Bacillus

CC subtilis".

CC Nature 390:249-256(1997).

CC -!- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic

CC linkages in glycogen by scission of a 1,4-alpha-linked

CC oligosaccharide from growing alpha-1,4-glucan chains and the

CC subsequent transfer of the oligosaccharide to other parts of

CC alpha-1,4-glucan chains.

CC -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of

CC glycogen.

CC -!- PATHWAY: Glycogen biosynthesis; third step.

CC -!- INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON

CC SOURCES THAT ALLOW EFFICIENT SPOULATION.

CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO

CC KNOWN AS THE ALPHA-AMYLASE FAMILY.

CC

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CC

CC EMBL; Z25795; CAAB1040.1; --

CC EMBL; AF008220; AAC00214.1; --

CC EMBL; Z99119; CAB15076.1; --

CC PIR; S40048; S40048.

CC Subtilist; BG10907; glgB.

CC InterPro; IPR006047; Alpha\_amyl\_cat.

CC InterPro; IPR006407; GlgB.

CC InterPro; IPR004193; Glyco\_hydro\_13N.

CC Pfam; PF00128; alpha-amylase; 1.

CC Pfam; PF02922; isoamylase; 1.

CC TIGRfam; TIGR01515; branching\_enzym; 1.

CC Glycogen biosynthesis; transferase; Glycosyltransferase;

CC Complete proteome.

CC ACT SITE 309 309 BY SIMILARITY.

CC ACT SITE 352 352 BY SIMILARITY.

CC ACT SITE 420 420 BY SIMILARITY.

CC SEQUENCE 627 AA; 73665 MW; 6480A553B6767BA CRC64;

Query Match 2.9%; Score 125; DB 1; Length 627;

Best Local Similarity 18.6%; Pred. No. 0.41;

Matches 131; Conservative 86; Mismatches 225; Indels 264; Gaps 37;

QY 49 NYNTNTEENVQNNMAGDKWSAFI-----KEOSTLAQMYPLOEIQNLTVKQLQALQON 103

DB 56 DFNSGSGEHRVHRVNDNGIWTLPFGIGKEK-----YKYEIVTN-----N 97

QY 104 GSSVLSEDKSKRLNLTNTMTSTYSTGKVCNPNPQECLELLEGLNEIMAN--SLDYNER 161

DB 98 GEIRLKADP-----YAIYS-----EVRENTASLTLDLE 125

QY 162 LWAWESRSEYKQLRPLYEYVVLKNEMARANHEDYGDYWRGDEYVANGVDGYDSRQ 221

DB 126 GYSWQDQKQKQAKTLXKPVFI-----YELHLGSMK-----KHSDGRHYSYKE 171

QY 222 LIEOV-----EHTFE--EIKPLYEHLHAYVRKLMNAYPSYISPIGCLPAHLGDMWGRF 274

DB 172 LSQTLIPYIKKHGTHIELPVYB--HPYDRS-----WGQY 205

QY 275 WTNLYSLTVPFQKPNIDVTDAWVDAQ-----WDAQRIFKEAEKFFVSVGLPNMT 324

DB 206 GTGYSPTSRFG--PPHDLN-KFVDECHQONIGVILDWVGFHFKDAHGLMDFGEP--- 259

QY 325 QGFVNSMLTDPGNVQKAVCHPTAWDJKGDFRILMCTKVTMDDELTAH----HEMCHIQ 380

DB 260 --LVEYKEERDEN-----WLGATNFDI----GKPEVHSFLISNLYAEFYHI- 303

QY 381 YDMAAQAQPLLRNANGNEGPH-EAVGIMSLSAATPKHLKSGILGLSPDFQEDNETEINFL 439

DB 304 -----DGFVDAVANILYWPNQDERH-----TNPYAVDFL 333

QY 440 LKQALITVGLTPTFTYML--EKWRWVFKGRI PKD-----QWKKWEMKRETVGVPEV 491

DB 334 KKLNTMEAPHYVMIAEDSTEPQVTGAVEGGLGFHYKWNMGW---MNDVLKWTETP 390

QY 492 PHDETCDPASLFFHVSNDYSPIRYTTLTYQFOQEAALCOAAKHEGLHKDCISNSTEAG 551

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Db 391 PEERRHC-----HQLISFSL-----YAFSEHFVLPFSDEVVY-----G 425
Qy 552 OKLFNMLRLKSGSPWTLALENVGAKMNVRLNAY-----FEPLFWLK 596
Db 426 KK--SLNKNPGDY-----QKFAQYRLLGLTWTHTPOKLLFMGSEFAQFDEW-K 473
Qy 597 DOWNKNSFVGSTWSPVADQSI-----KYRISLSKALGKAYEND-----NEWYL 642
Db 474 DTEQ---LDWFLDSFFMHOKASVFTODLLRFYQKSKILYEHDDHRAQSPENIDVHNDQSI 530
Qy 643 FRSSVAYAMROYELKVKQNMILFGEDVRVANLKRISFNFFVTAP 688
Db 531 F-SPIRYGQKH-----GEALVLIICNFTPVWYHQYDVGVP 563

RESULT 13
ID EP1B STABP STANDARD; PRT; 986 AA.
AC P30195;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Epidermin biosynthesis protein ep1B.
GN EP1B.
OS Staphylococcus epidermidis.
CG Plasmid pTU 32.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TU 3298 / DSM 3095;
RX MEDLINE=92155237; PubMed=1740156;
RA Schnell N., Engelke G., Augustin J., Rosenstein R., Ungermann V.,
RT "Analysis of genes involved in the biosynthesis of lantibiotic
epidermin."
RL Eur. J. Biochem. 204:57-68(1992).
CC -!- FUNCTION: INVOLVED IN THE POSTTRANSLATIONAL MODIFICATION OF THE
LANTIBIOTIC EPIDERMIN.
CC -!- SUBCELLULAR LOCATION: POSSIBLY ASSOCIATED WITH, AND ANCHORED TO,
THE CYTOPLASMIC SIDE OF THE MEMBRANE.
CC -!- SIMILARITY: TO B.SUBTILIS SPAB AND L.LACTIS NISB.

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EMBL; X62386; CAA44253.1;
DR InterPro; IPR006827; Lant_dehyd_C.
DR InterPro; IPR006826; Lant_dehyd_N.
DR Pfam; PF04739; Lant_dehyd_C; 1.
DR Pfam; PF04737; Lant_dehyd_N; 1.
KW Plasmid.
SQ SEQUENCE 986 AA; 116708 MW; 343CE98526847850 CRC64;

Query March 2.98; Score 123; DB 1; Length 986;
Best Local Similarity 18.28; Pred. No. 1.1; Mismatches 258; Indels 310; Gaps 40;
Matches 153;

Qy 1 MSSSSWLLSLVAVTAAQSTIEQAKTFLDKFNHE-----ABDL--FYQSSLAGWNY 50
Db 320 ISEAAVILMLLSPNHFQTKTIRNYHEFFMDKYGFQQLVNLKQLLSDINGFGYKKDSYVF 379
Qy 51 NNTNTEENVQNMNAGDKWAFKESQSLAQMYPLOEQNLTKLQALQONGSSVLSE 110
Db 380 SNNI-----AFLEK-----YLAIGNSHIEITE 404
Qy 111 DKSKRLNTLNTSTIYTGKVCNPDNPQECILLEPGLMEIMANSIDYNERLAWESWRS 170
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Db 405 NDVKNLEK--NNTVSKINA-----PVSTEI-----YSEIYF----- 433
Qy 171 EVGQQLRPLYEYVVLKXEMARAHYEDYCDYWRGDEYVNGVDYDYSRQGLIEDVEHTF 230
Db 434 --GNSIKG--YEDFAVISPIIGSFNAGATGFRF--TGNFNK-----KNQLOKEIVH-- 480
Qy 231 BEIKPLVEHLHAYYRAKLMNAYPSYISPIGCLPAHLLGDMGGRFTWNLVSLYVPGQKPN 290
Db 481 -----HNNYMNENGLBISQINBGLNSRNVNLIANN--NRIYNTCLNLNLP-----KSD 527
Qy 291 IDVTDMVDQAWDAQRIFKE---AEKFFVSVGLPNMTQ-----FWNSMLTDPG 337
Db 528 IDINDIFIGATFNKLYLYSEKHSRIVFVSNSMFNFEFGSELYKFLREISFEKTKFIQPI 587
Qy 338 N-----VOKAVCHPTAWDLKSGDFRILMCTKVMTDDFLTAHHEGHQIDM 383
Db 588 TEEGIDSLFPCPRIIYKNILKPKATWKINSEMFSE---TENMLNRPATI--REKWHIPKDV 643
Qy 384 AYA-----AQPFLRNGANEGFHEAVGEIMS----- 409
Db 644 IIAFGDNRLNLLNLDKHLIILKELKCHGRIRILESFINESNNRMLEIVTPLYKKTSL 703
Qy 410 --LSAATPK-----HLK--SIGLLSPDFQEDNETEINELLKQALTIVGTLPTMYLE 457
Db 704 KEQSFILPKNRKHNKFNLLKOWFSLHSIPKTYQD-----NFIQDYLLPFIETELKNNFIN 758
Qy 458 KRWNVFKGEIPKQDMKQKWMKREIVGVVPEVPHDETICDPASLFHVSNDYSIRYY- 516
Db 759 KFFYIKFKED---EDFIK--LRLIRE-----DEDY-----SQIYSFKKNWK 794
Qy 517 -----TRTYQFOFEALCOAAKHGPHLHKDISNSTEAGQKLFNMLRLGKSEPTWLALE 571
Db 795 DYCLNLSLDYSIVDVVPEVRYGSPHYVEDIENFFMYDSL--SINIQSE-FKIPKE 851
Qy 572 NVGAKMNVRLNLYPEPLFTWLKQONKNSFVGWSTWSPYADQSIKVRISLKGALGDK 631
Db 852 FIVA---ISIDFLDYLE-----INKEKEEILINNA--ED 882
Qy 632 AYEWNDNMYLFRSSVAYAMROYFLKVKQNMILFGEDVRVANLKRISFNFFVTAPKTV 691
Db 883 LYRSD-----IREY-----KNLLAKL-----TNPKND 905
Qy 632 SDLP-----RTEVEKATRMSRINDAF-----RLNDSLSFLGIQ 728
Db 906 YEILKGFNNLHEFLFNKISILENLKTKLQSLYTSRSRIIGSFHMRCN-----RIFGIN 961
Qy 729 P 729
Db 962 P 962

RESULT 14
EGAL_BACME STANDARD; PRT; 1034 AA.
ID EGAL_BACME
AC O52847;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Beta-galactosidase (EC 3.2.1.23) (Lactase).
GN BGAM.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 319;
RA Strept J.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
galactose residues in beta-D-galactosides.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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[illegible]

Search completed: February 19, 2004, 19:50:14  
Job time : 21 secs



XX 29-SEP-1999; 99WO-US22976.  
 XX 30-SEP-1999; 98US-0163648.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Acton LS, Robison KE, Hsieh FV;  
 XX WPI; 2000-293140/25.  
 XX N-PSDB; AA12764.  
 CC isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)  
 CC polypeptide useful for detecting an ACE-2 therapeutic for treating  
 CC hypertension, congestive heart failure, myocardial infarction,  
 CC atherosclerosis and renal failure.  
 CC  
 CC Claim 2; Fig 1; 138pp; English.  
 CC The present sequence represents a human angiotensin converting enzyme-2  
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The  
 CC sequence of the full length ACE-2 cDNA was determined from a clone  
 CC obtained from a cDNA library prepared from mRNA of a human heart of  
 CC a subject who had congestive heart failure. ACE-2 has significant  
 CC sequence homologies with ACE enzymes, and has also been shown to  
 CC hydrolyse angiotensin I into Ang (1-9). The ACE-2 therapeutics are  
 CC used to treat blood pressure related diseases and conditions, such as  
 CC hypertension, congestive heart failure, chronic heart failure, acute  
 CC heart failure, myocardial infarction, atherosclerosis and renal  
 CC failure.  
 CC  
 CC SQ Sequence 805 AA;  
 \* Query Match 100.0%; Score 4291; DB 21; Length 805;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSSSSWLLSLVAVTAQAOSTIEEQAKTFLDKFNHEADLFYQSSLASWNTNITEENVQ 60  
 DB 1 MSSSSWLLSLVAVTAQAOSTIEEQAKTFLDKFNHEADLFYQSSLASWNTNITEENVQ 60  
 QY 61 NMNAGDKWSAFLKEQSTLAQMYPLQEIQLNVLKQLQALQNGSSVLSKSLRNLTL 120  
 DB 61 NMNAGDKWSAFLKEQSTLAQMYPLQEIQLNVLKQLQALQNGSSVLSKSLRNLTL 120  
 QY 121 NTWSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180  
 DB 121 NTWSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180  
 QY 181 EYVVLKNEMARANHYEDYDGYWRGDEYVNGVDYSGQLIEDVHTFEEIKPLYEHL 240  
 DB 181 EYVVLKNEMARANHYEDYDGYWRGDEYVNGVDYSGQLIEDVHTFEEIKPLYEHL 240  
 QY 241 HAYVRALKNMAYPSYISPIGCLPAHLGDMGWFNTLSLVTPFGQKPNIDVTDAMVDQ 300  
 DB 241 HAYVRALKNMAYPSYISPIGCLPAHLGDMGWFNTLSLVTPFGQKPNIDVTDAMVDQ 300  
 QY 301 AWDQRIFXEAKEKFFSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLKGDFRILM 360  
 DB 301 AWDQRIFXEAKEKFFSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLKGDFRILM 360  
 QY 361 CTKVTMDDELTAHHEMGHIQYDWAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
 DB 361 CTKVTMDDELTAHHEMGHIQYDWAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
 QY 421 IGLLSPPQEDNETEINFLKQALITVGTLPFFYMLEKRWVMVFKEIPKQDMKKWEM 480  
 DB 421 IGLLSPPQEDNETEINFLKQALITVGTLPFFYMLEKRWVMVFKEIPKQDMKKWEM 480  
 QY 481 KREIVGVVPEVPHDETCDPASLPHVSNDSYFRTYTRILYQFOFQALCOAAKEGPHL 540  
 DB 481 KREIVGVVPEVPHDETCDPASLPHVSNDSYFRTYTRILYQFOFQALCOAAKEGPHL 540

QY 541 KCDISNSTEAGQKLFNMLRLGKSEPTWLTALENVVGAKNNVRPLLNVFFPLFTWLKDQNK 600  
 DB 541 KCDISNSTEAGQKLFNMLRLGKSEPTWLTALENVVGAKNNVRPLLNVFFPLFTWLKDQNK 600  
 QY 601 NSFVGWSTDSFYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAVAMROYFLKVK 660  
 DB 601 NSFVGWSTDSFYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAVAMROYFLKVK 660  
 QY 661 QMILFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720  
 DB 661 QMILFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720  
 QY 721 SLEFLIGIOTLPNPNQPPSVLWLVFGVGMGVIVGVILIFGTGIDRKKKNGKARSENP 780  
 DB 721 SLEFLIGIOTLPNPNQPPSVLWLVFGVGMGVIVGVILIFGTGIDRKKKNGKARSENP 780  
 QY 781 YASIDISKGENNPGFQNTDDVQTSF 805  
 DB 781 YASIDISKGENNPGFQNTDDVQTSF 805  
 RESULT 2  
 AAY67310  
 ID AAY67310 standard; Protein; 805 AA.  
 XX AAY67310;  
 AC AAY67310;  
 XX 11-APR-2000 (first entry)  
 DT Human MPROT15 amino acid sequence #1.  
 DE MPROT15; treatment; hypertension; human; myocardial disease; apoplexy;  
 XX heart disease; apoplexy; heart disease; nervous denaturation; hormone;  
 KW Alzheimer's disease; cytokine.  
 XX Homo sapiens.  
 XX JPL1318472-A.  
 XX 24-NOV-1999.  
 XX 22-JAN-1999; 99JP-0014949.  
 XX 13-MAY-1998; 98GB-0010373.  
 XX 18-AUG-1998; 98GB-0018009.  
 XX (SMIK) SMITHKLINE BEECHAM PLC.  
 XX WPI; 2000-109268/10.  
 XX N-PSDB; AA259465.  
 XX MPROT15 polypeptide and MPROT15 polynucleotides - useful for the  
 XX treatment of hypertension, myocardial diseases, apoplexy, heart  
 XX diseases, nervous denaturation, Alzheimer's disease etc.  
 XX Claim 1; Page 15; 22pp; Japanese.  
 XX This is amino acid sequence #1 of human MPROT15. The MPROT15  
 XX polynucleotide and polypeptide sequences can be used for the treatment of  
 XX hypertension, myocardial diseases, apoplexy, heart diseases, nervous  
 XX denaturation, Alzheimer's disease and diseases related to the processing  
 XX of peptide hormones and cytokines.  
 XX Sequence 805 AA;  
 Query Match 100.0%; Score 4291; DB 21; Length 805;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSSSSWLLSLVAVTAQAOSTIEEQAKTFLDKFNHEADLFYQSSLASWNTNITEENVQ 60  
 DB 1 MSSSSWLLSLVAVTAQAOSTIEEQAKTFLDKFNHEADLFYQSSLASWNTNITEENVQ 60

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QY 61 NMNAGDKWSAFLEKQSTLAQMYPIQETONLTVKQLQALQONGSSVLSSEKSKRLNTIL 120
Db 61 NMNAGDKWSAFLEKQSTLAQMYPIQETONLTVKQLQALQONGSSVLSSEKSKRLNTIL 120
QY 121 NTMSTIYSTGKVCNPDNPOECLELLEPGLNEIMANSLDYNELNMAWESRSEVKGQRLPLY 180
Db 121 NTMSTIYSTGKVCNPDNPOECLELLEPGLNEIMANSLDYNELNMAWESRSEVKGQRLPLY 180
QY 181 EYVVLKEMARANEHYEDYDYGWDYEVNGVDGYDYSRGQLIEDVEHTEFEIKPLYEHL 240
Db 181 EYVVLKEMARANEHYEDYDYGWDYEVNGVDGYDYSRGQLIEDVEHTEFEIKPLYEHL 240
QY 241 HAYVRAKLNNAYPSYISPIGCLPAHLGLDMMGRFWTNLYSLTVPFQKPNIDVTDAVDQ 300
Db 241 HAYVRAKLNNAYPSYISPIGCLPAHLGLDMMGRFWTNLYSLTVPFQKPNIDVTDAVDQ 300
QY 301 ANDAQRIFKEAEKFFVSGLPNMTQGFWENSMITDPGNVQKAVCHPTAWDLGKDFRILM 360
Db 301 ANDAQRIFKEAEKFFVSGLPNMTQGFWENSMITDPGNVQKAVCHPTAWDLGKDFRILM 360
QY 361 CTKVMTDDPLTAHMGHIQDYMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
Db 361 CTKVMTDDPLTAHMGHIQDYMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
QY 421 IGLSPDFQEDNETEINFLLQAALTIQVTLPTFTYMLEKRWMMVFKEIPEKQOMMKWEM 480
Db 421 IGLSPDFQEDNETEINFLLQAALTIQVTLPTFTYMLEKRWMMVFKEIPEKQOMMKWEM 480
QY 481 KKEIVGVVEPVPHDQETCDPASLPHVSNDSYFIRYTRTYQFQFQALCOAAKHEGPH 540
Db 481 KKEIVGVVEPVPHDQETCDPASLPHVSNDSYFIRYTRTYQFQFQALCOAAKHEGPH 540
QY 541 KCDISNSTEAGOKLFNMLRLKSEFPWTLALENVGAKNMVRLNLYFFELFTWLKQNK 600
Db 541 KCDISNSTEAGOKLFNMLRLKSEFPWTLALENVGAKNMVRLNLYFFELFTWLKQNK 600
QY 601 NSFVGSWSDMSYADOSIKVRSLSKALGDKAVENWNNEMVLPSSVAVAMQYFLKVN 660
Db 601 NSFVGSWSDMSYADOSIKVRSLSKALGDKAVENWNNEMVLPSSVAVAMQYFLKVN 660
QY 661 QMILFGEEDVRVANKPRISNFFVTAPKNVSDIIPRTEVEKAIKMSRINDAFRLND 720
Db 661 QMILFGEEDVRVANKPRISNFFVTAPKNVSDIIPRTEVEKAIKMSRINDAFRLND 720
QY 721 SLEFLGIQPTLGPNNQPPVSLWLVFGVWGVIVGIVILIETGIRDRKKNKASGENP 780
Db 721 SLEFLGIQPTLGPNNQPPVSLWLVFGVWGVIVGIVILIETGIRDRKKNKASGENP 780
QY 781 YASIDISKGNPNPGFQNTDDVQTSF 805
Db 781 YASIDISKGNPNPGFQNTDDVQTSF 805

RESULT 3
ID AAY72667 standard; Protein; 805 AA.
XX AC AAY72667;
XX DT 31-MAY-2001 (first entry)
XX DE Human angiotensin converting enzyme-2 (ACE-2).
XX KW Human; angiotensin converting enzyme-2; ACE-2; peptidyl dipeptidase A;
XX KW screening; therapy; hypertension; congestive heart failure; CHF;
XX KW inflammation; pain.
XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT 1..18
XX FT /label= Signal_peptide
XX FT 19..805

```

```

FT Domain
FT /label= Mature_ACE-2_protein
FT 374..378
FT /label= ZBD
FT /note= "Zinc binding domain"
FT 741..765
FT /label= TMD
FT /note= "Transmembrane domain; Hydrophobic region"
FT 766..805
FT /label= Cytoplasmic_domain
FN US6194556-B1.
PD 27-FEB-2001.
XX PF 11-DEC-1997; 97US-0989299.
XX PR 11-DEC-1997; 97US-0989299.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Acton SL, Robison KE;
XX WP; 2001-210604/21.
XX DR N-PSDB; AAD02758.
XX PT Novel genes encoding angiotensin converting enzyme-2 useful as
XX PT antisense or antigene agents for therapeutics, diagnostics and
XX PS screening assays.
XX Claim 33; Fig 1; 76pp; English.
CC The present amino acid sequence is human angiotensin converting enzyme-2
CC (ACE-2), also referred as peptidyl dipeptidase A (EC 3.4.15.1). Nucleic
CC acid sequence encoding ACE-2 is useful as antisense or antigene agents
CC for sequence specific modulation of gene expression or in the analysis of
CC single base-pair mutations in the gene. Nucleic acid sequence encoding
CC ACE-2 is useful in therapeutics, diagnostics and in screening assays.
CC ACE-2 antagonist is used to treat hypertension or congestive heart
CC failure (CHF). ACE agonist is used to reduce the inflammation and pain
CC resulting from an insect sting or bite, which was accompanied by an
CC injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2
CC protein levels for determining the disease or condition associated with
CC an aberrant protein level.
XX SQ Sequence 805 AA;

```

```

Query Match 100.0%; Score 4291; DB 22; Length 805;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEADLFYQSSLASWNYNTNITEENVQ 60
Db 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEADLFYQSSLASWNYNTNITEENVQ 60
QY 61 NMNAGDKWSAFLEKQSTLAQMYPIQETONLTVKQLQALQONGSSVLSSEKSKRLNTIL 120
Db 61 NMNAGDKWSAFLEKQSTLAQMYPIQETONLTVKQLQALQONGSSVLSSEKSKRLNTIL 120
QY 121 NTMSTIYSTGKVCNPDNPOECLELLEPGLNEIMANSLDYNELNMAWESRSEVKGQRLPLY 180
Db 121 NTMSTIYSTGKVCNPDNPOECLELLEPGLNEIMANSLDYNELNMAWESRSEVKGQRLPLY 180
QY 181 EYVVLKEMARANEHYEDYDYGWDYEVNGVDGYDYSRGQLIEDVEHTEFEIKPLYEHL 240
Db 181 EYVVLKEMARANEHYEDYDYGWDYEVNGVDGYDYSRGQLIEDVEHTEFEIKPLYEHL 240
QY 241 HAYVRAKLNNAYPSYISPIGCLPAHLGLDMMGRFWTNLYSLTVPFQKPNIDVTDAVDQ 300
Db 241 HAYVRAKLNNAYPSYISPIGCLPAHLGLDMMGRFWTNLYSLTVPFQKPNIDVTDAVDQ 300
QY 301 ANDAQRIFKEAEKFFVSGLPNMTQGFWENSMITDPGNVQKAVCHPTAWDLGKDFRILM 360
Db 301 ANDAQRIFKEAEKFFVSGLPNMTQGFWENSMITDPGNVQKAVCHPTAWDLGKDFRILM 360

```



QY 361 CTXVTMDDFLTAHENGHIQYDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKS 420  
 Db 361 CTXVTMDDFLTAHENGHIQYDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKS 420  
 QY 421 IGLLSPDFQEDNETEINFLKQALTIIVGTLPTTYMLEKRWVVFKEIPKQWKKWEM 480  
 Db 421 IGLLSPDFQEDNETEINFLKQALTIIVGTLPTTYMLEKRWVVFKEIPKQWKKWEM 480  
 QY 481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTLTQFQOEALCOAAKHEGPLH 540  
 Db 481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTLTQFQOEALCOAAKHEGPLH 540  
 QY 541 KCDISNSTEAGQKLFNNLRGKSEPTWTLAENNVGAKNNVRPLLYPEPFTWLKQNK 600  
 Db 541 KCDISNSTEAGQKLFNNLRGKSEPTWTLAENNVGAKNNVRPLLYPEPFTWLKQNK 600  
 QY 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVK 660  
 Db 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVK 660  
 QY 661 QMILFGEEDYRVANLKPRISENFVTPAKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720  
 Db 661 QMILFGEEDYRVANLKPRISENFVTPAKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720  
 QY 721 SLFELGIQPTLGPNNOPPVSIIMLVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 780  
 Db 721 SLFELGIQPTLGPNNOPPVSIIMLVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 780  
 QY 781 YASIDISKGNNPQNTDDVQTSF 805  
 Db 781 YASIDISKGNNPQNTDDVQTSF 805

## RESULT 4

AAB48095

ID AAB48095 standard; Protein; 805 AA.

AC AAB48095;

DT 19-MAR-2001 (first entry)

DE Human Zace2 protein.

KW Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;  
 KW zinc metalloproteinase; blood pressure; zinc protease; hypertension;  
 KW ventricular systolic dysfunction; renal impairment; heart failure;  
 KW scleroderma renal crisis; atherosclerosis; anti-inflammatory; human;  
 KW antiarthritic; bradykinin inactivator.

OS Homo sapiens.

PN WO200070032-A1.

PD 23-NOV-2000.

PF 03-MAY-2000; 2000WO-US11932.

PR 13-MAY-1999; 99US-0311482.

PR 27-AUG-1999; 99US-0384706.

PA (ZYMO) ZYMOGENETICS INC.

PI Piddington CS, Petrie CR, Shoemaker KE, Bishop PD;

DR WPI; 2001-025018/03.

DR N-FSD8; AAC84366, AAC84367.

XX Angiotensin-converting enzyme, Zace2, useful for treating inflammatory  
 PT bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases  
 PT associated with inflammation such as arthritis and enterocolitis -

XX Example 1; Page 95-100; 125pp; English.

XX The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-  
 CC converting enzyme is a zinc metalloproteinase that plays roles in blood  
 CC pressure regulation and fertility. Zace2 can be expressed by standard  
 CC recombinant methodology. Zace2 polypeptides are useful for treating an  
 CC inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),  
 CC diseases associated with inflammation like arthritis and enterocolitis,  
 CC as targets for identifying modulators of zinc protease activity, for  
 CC screening for identifying new angiotensin-converting enzyme (ACE)  
 CC inhibitors, and as a basis for rational drug design for inhibitory  
 CC molecules. The nucleic acids can be used to detect the expression of a  
 CC Zace2 gene in a biological sample, as probes for in vivo diagnosis and  
 CC for detecting and localizing Zace2 gene expression in tissue samples,  
 CC to determine whether a subject's chromosomes contain a mutation in the  
 CC Zace2 gene, and to detect aberrations associated with the Zace2 locus.  
 CC Inhibitors of ACE are used for treating hypertension of various  
 CC conditions, including left ventricular systolic dysfunction, progressive  
 CC renal impairment, scleroderma renal crisis, congestive heart failure due  
 CC to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be  
 CC used to treat infertility while Zace2 antagonists are used for inducing  
 CC infertility. The present sequence represents the human Zace2 protein.  
 CC  
 XX Sequence 805 AA;

Query Match 100.0%; Score 4291; DB 22; Length 805;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVATAAQSTIEQAKTFLDKFNHEADLFYQSSLASWYNNYNTNENVQ 60  
 Db 1 MSSSSWLLLSLVATAAQSTIEQAKTFLDKFNHEADLFYQSSLASWYNNYNTNENVQ 60  
 QY 61 NNNNAGDKWSAFLKEQSTLAQMYPLQIQLVTKLQALQALQNGSSVLSEKSLNTIL 120  
 Db 61 NNNNAGDKWSAFLKEQSTLAQMYPLQIQLVTKLQALQALQNGSSVLSEKSLNTIL 120  
 QY 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSIDYNERLWAMESWSEVKQLRPY 180  
 Db 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSIDYNERLWAMESWSEVKQLRPY 180  
 QY 181 EYVVLKNEMARANHYEDYDYGWRGDEYVNGVDYDYSRGQLIEDVEHTFEIKLYEHL 240  
 Db 181 EYVVLKNEMARANHYEDYDYGWRGDEYVNGVDYDYSRGQLIEDVEHTFEIKLYEHL 240  
 QY 241 HAYVRKLMWAPSYIPIGCLPAHLGDMWGFNTNLYSLTVPFGKPNIDVTAMDQ 300  
 Db 241 HAYVRKLMWAPSYIPIGCLPAHLGDMWGFNTNLYSLTVPFGKPNIDVTAMDQ 300  
 QY 301 AWDAQRIFKEAEKPFVSVGLPNNMTQGFWNSMLTDFGNVQKAVCHPTAMDLGKGFRIIM 360  
 Db 301 AWDAQRIFKEAEKPFVSVGLPNNMTQGFWNSMLTDFGNVQKAVCHPTAMDLGKGFRIIM 360  
 QY 361 CTKVTMDDFLTAHENGHIQYDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKS 420  
 Db 361 CTKVTMDDFLTAHENGHIQYDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKS 420  
 QY 421 IGLLSPDFQEDNETEINFLKQALTIIVGTLPTTYMLEKRWVVFKEIPKQWKKWEM 480  
 Db 421 IGLLSPDFQEDNETEINFLKQALTIIVGTLPTTYMLEKRWVVFKEIPKQWKKWEM 480  
 QY 481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTLTQFQOEALCOAAKHEGPLH 540  
 Db 481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTLTQFQOEALCOAAKHEGPLH 540  
 QY 541 KCDISNSTEAGQKLFNNLRGKSEPTWTLAENNVGAKNNVRPLLYPEPFTWLKQNK 600  
 Db 541 KCDISNSTEAGQKLFNNLRGKSEPTWTLAENNVGAKNNVRPLLYPEPFTWLKQNK 600  
 QY 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVK 660  
 Db 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVK 660  
 QY 661 QMILFGEEDYRVANLKPRISENFVTPAKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720

Db 661 QMLGGEEDVAVANLKPRISNFFVTAPKXVSDIIPTEVEKAIMSRSSINDAFRLNDN 720  
 QY 721 SLEFGLIGIOTLGPNNQPPVSLWLVFVGMGVVGVVILFTGIRDKKKNKARGSENP 780  
 Db 721 SLEFGLIGIOTLGPNNQPPVSLWLVFVGMGVVGVVILFTGIRDKKKNKARGSENP 780  
 QY 781 YASIDISKGNPNPGFQNTDDVQTSF 805  
 Db 781 YASIDISKGNPNPGFQNTDDVQTSF 805  
 RESULT 5  
 ABG77011  
 ID ABG77011 standard; Protein; 805 AA.  
 AC ABG77011;  
 XX  
 DT 05-NOV-2002 (first entry)  
 DE Human angiotensin converting enzyme 2.  
 XX  
 KW Aminopeptidase P; XNPEP2; bradykinin receptor B1;  
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;  
 KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
 KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KW myocardial infarction; ventricular hypertrophy; vascular disease;  
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 KW autoimmune disease; inflammatory arthritis; cancer; wound;  
 KW viral infection; bacterial infection; fungal infection; COPD;  
 KW Chronic obstructive pulmonary disease; enterocolitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261131-A2.  
 PP  
 PF 09-AUG-2002.  
 PF 03-DEC-2001; 2001WO-US47235.  
 XX 04-DEC-2000; 2000US-251015P.  
 PR 23-JAN-2001; 2001US-263678P.  
 PR 02-MAR-2001; 2001US-273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/L) HUI L.  
 XX  
 PI Tauchihasi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 XX  
 DR WPI; 2002-619265/66.  
 DR N-PSDB; ABS60372.  
 XX  
 PT New isolated nucleic acid with at least one polymorphic position,  
 PT useful for detecting, diagnosing and treating disorders such as  
 PT angioedema, cancer, viral, bacterial or fungal infection,  
 PT cardiovascular and autoimmune diseases -  
 XX  
 PS Disclosure; Fig 32; 977pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XNPEP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic  
 CC acids; (4) identifying (M3) an individual at risk of developing a  
 CC disorder upon administration of an ACE inhibitor and/or vasopeptidase  
 CC inhibitor using the polymorphic data; (5) a library of nucleic acids,  
 CC each of which comprises one or more polymorphic positions within a gene  
 CC encoding a human protein selected from the group above; and (6)  
 CC genotyping (M4) an individual comprising obtaining a nucleic acid sample,  
 CC determining the nucleotide present in at least one polymorphic position,  
 CC and comparing at least one position with a known data set. The genes,  
 CC (M1, M2, M3 and M4) and compositions are useful for detecting,  
 CC diagnosing, treating, preventing various disorders such as angioedema  
 CC and diseases which involve angiogenesis like haemangiomas, tumours,  
 CC sarcomas, Crohn's disease, trachoma, and cardiovascular diseases like  
 CC angina pectoris, hypertension, heart failure, myocardial infarction,  
 CC ventricular hypertrophy, vascular diseases, aneurysm, embolism,  
 CC thrombosis, coronary artery disease, arteriosclerosis and/or  
 CC atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune  
 CC diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or  
 CC fungal infection, Chronic obstructive pulmonary disease (COPD) and  
 CC enterocolitis (many other diseases and disorders are listed in the  
 CC specification). The polymucleotides are also useful for chromosome  
 CC identification. Antibodies against the proteins may be utilised for  
 CC immunophenotyping of cell lines and biological samples. The present  
 CC sequence represents one of the proteins listed above.  
 XX  
 SQ Sequence 805 AA;  
 Query Match 100.0%; Score 4291; DB 23; Length 805;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSSSSWLLLSLVAVTAAQSTIEQAKTFELDKFNHEADLFYQSSLASWYNTNTEENVQ 60  
 Db 1 MSSSSWLLLSLVAVTAAQSTIEQAKTFELDKFNHEADLFYQSSLASWYNTNTEENVQ 60  
 QY 61 MNVAGDKWSAFLKEQSTLAQMYPLQEIQNLTKVQLQALQNGSSVLSDESKRLNTLL 120  
 Db 61 MNVAGDKWSAFLKEQSTLAQMYPLQEIQNLTKVQLQALQNGSSVLSDESKRLNTLL 120  
 QY 121 NTMSTIYSTGKVCNPNPQECLELLEPCLNEMANSIDYNERLWAWESWSEVKGKLRPLY 180  
 Db 121 NTMSTIYSTGKVCNPNPQECLELLEPCLNEMANSIDYNERLWAWESWSEVKGKLRPLY 180  
 QY 181 EYVVLKNEWARANHYEDYGYWRGDEYVNGVDGYDSRGQIEDVEHTFBEIKPLYEHL 240  
 Db 181 EYVVLKNEWARANHYEDYGYWRGDEYVNGVDGYDSRGQIEDVEHTFBEIKPLYEHL 240  
 QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLLDGMWGFNTNLYSLTVPFQCKENIDVTDAMVDQ 300  
 Db 241 HAYVRAKLMNAYPSYISPIGCLPAHLLDGMWGFNTNLYSLTVPFQCKENIDVTDAMVDQ 300  
 QY 301 AWDAQRIFKEAEKFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLM 360  
 Db 301 AWDAQRIFKEAEKFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLM 360  
 QY 361 CTKVYTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGIMSLSAATPHLKS 420  
 Db 361 CTKVYTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGIMSLSAATPHLKS 420  
 QY 421 IGLLSPDFQEDNETEINFILKQALITVGTLPFFYMLKRWVFWVFKGEIPDQNMKKNWEM 480  
 Db 421 IGLLSPDFQEDNETEINFILKQALITVGTLPFFYMLKRWVFWVFKGEIPDQNMKKNWEM 480  
 QY 481 KREIVGVVPEVPHDDETCDPASLFHVSNDYSFIRYVTRTLTYQFQFQALCOAAKHEGPLH 540  
 Db 481 KREIVGVVPEVPHDDETCDPASLFHVSNDYSFIRYVTRTLTYQFQFQALCOAAKHEGPLH 540  
 QY 541 KCDISNSTEAGOKLFNMLRKGSEPTALENVVGAKNMVRPLNLYFPLFTWLKDQNK 600  
 Db 541 KCDISNSTEAGOKLFNMLRKGSEPTALENVVGAKNMVRPLNLYFPLFTWLKDQNK 600

QY 601 NSFVGSWTDSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAVAMEQYFLKYN 660  
 Db 601 NSFVGSWTDSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAVAMEQYFLKYN 660  
 QY 661 QMILFGEEDVRANLKRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFLNDN 720  
 Db 661 QMILFGEEDVRANLKRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFLNDN 720  
 QY 721 SLEFLIGTOPTGPNOPPVSWLIVFGVWGVWGIIVLIFGIDRKKKAKSGENP 780  
 Db 721 SLEFLIGTOPTGPNOPPVSWLIVFGVWGVWGIIVLIFGIDRKKKAKSGENP 780  
 QY 781 YASIDISKGENNPGFQNTDDVQTSF 805  
 Db 781 YASIDISKGENNPGFQNTDDVQTSF 805

RESULT 5  
 ABG77023  
 ID ABG77023 standard; Protein; 805 AA.  
 XX  
 AC ABG77023;  
 DT  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human angiotensin converting enzyme 2 variant #1.  
 XX  
 XX Aminopeptidase P; XNBP2; bradykinin receptor B1; human;  
 XX BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;  
 XX kallikrein 1; KUK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
 XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 XX cardiovascular disease; angina pectoris; hypertension; heart failure;  
 XX myocardial infarction; ventricular hypertrophy; vascular disease;  
 XX aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
 XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 XX autoimmune disease; inflammatory arthritis; cancer; wound;  
 XX viral infection; bacterial infection; fungal infection; COPD;  
 XX Chronic obstructive pulmonary disease; enterocolitis.  
 OS Homo sapiens.  
 XX  
 XX WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US47235.  
 XX  
 PR 04-DEC-2000; 2000US-251015P.  
 PR 23-JAN-2001; 2001US-263678P.  
 PR 02-MAR-2001; 2001US-273037P.  
 XX  
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 XX  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 PI WPI; 2002-619265/66.  
 DR NPSDB; ABS60633.  
 XX  
 XX New isolated nucleic acid with at least one polymorphic position,  
 PT useful for detecting, diagnosing and treating disorders such as  
 PT angioedema, cancer, viral, bacterial or fungal infection,  
 PT cardiovascular and autoimmune diseases -  
 XX  
 PS Disclosure; Fig 37; 977pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XNBP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein

CC 1 (KUK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic  
 CC acids; (4) identifying (M3) an individual at risk of developing a  
 CC disorder upon administration of an ACE inhibitor and/or vasopeptidase  
 CC inhibitor using the polymorphic data; (5) a library of nucleic acids,  
 CC each of which comprises one or more polymorphic positions within a gene  
 CC encoding a human protein selected from the group above; and (6)  
 CC genotyping (M4) an individual comprising obtaining a nucleic acid sample,  
 CC determining the nucleotide present in at least one polymorphic position,  
 CC and comparing at least one position with a known data set. The genes,  
 CC (M1, M2, M3 and M4) and compositions are useful for detecting,  
 CC diagnosing, treating, preventing various disorders such as angiodaema  
 CC and diseases which involve angiogenesis like haemangiomas, tumours, and  
 CC sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like  
 CC angina pectoris, hypertension, heart failure, myocardial infarction,  
 CC ventricular hypertrophy, vascular diseases, aneurysm, embolism,  
 CC thrombosis, coronary artery disease, arteriosclerosis and/or  
 CC diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or  
 CC fungal infection, Chronic obstructive pulmonary disease (COPD) and  
 CC enterocolitis (many other diseases and disorders are listed in the  
 CC specification). The polymorphisms are also useful for chromosome  
 CC identification. Antibodies against the proteins may be utilised for  
 CC immunophenotyping of cell lines and biological samples. The present  
 CC sequence represents a polymorphic variant of one of the proteins listed  
 CC above.

XX SQ Sequence 805 AA;

Query Match 100.0%; Score 4291; DB 23; Length 805;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAQSTIEQAKTFLDKFNEAEDLFYQSSLASWYNTNITEENVQ 60

Db 1 MSSSSWLLLSLVAVTAAQSTIEQAKTFLDKFNEAEDLFYQSSLASWYNTNITEENVQ 60

QY 61 NVNAGDKWSAFLKEOSTLAQMYELOIQLTKLQLOALQNGSSVLGDSKRLNTIL 120

Db 61 NVNAGDKWSAFLKEOSTLAQMYELOIQLTKLQLOALQNGSSVLGDSKRLNTIL 120

QY 121 NTMSTIYTGKVCNPNPQECCLLEPGLNEIMANSLDYNERLWAWESWSEVGKQLRPLY 180

Db 121 NTMSTIYTGKVCNPNPQECCLLEPGLNEIMANSLDYNERLWAWESWSEVGKQLRPLY 180

QY 181 EBYVVLKNEMARANHEDYGDYWGVDYNGVDYSGQLLEDVEHTFEETKPLYEHL 240

Db 181 EBYVVLKNEMARANHEDYGDYWGVDYNGVDYSGQLLEDVEHTFEETKPLYEHL 240

QY 241 HAYVRAKLNNAYPSYISPGICLPAHLGDMWRFTWNLVSLTVPFGKPNIDVTDAMVQ 300

Db 241 HAYVRAKLNNAYPSYISPGICLPAHLGDMWRFTWNLVSLTVPFGKPNIDVTDAMVQ 300

QY 301 AMDAQRIFKEAEKFPVSUPLNMTQGWENSMITDPGNVQKAVCHPTAMDGLGDFRILM 360

Db 301 AMDAQRIFKEAEKFPVSUPLNMTQGWENSMITDPGNVQKAVCHPTAMDGLGDFRILM 360

QY 361 CTKVMTDDFLTAHEMGIHQYDMAYAAQPFLLRNGANEFGHEAVGIMSLSATPKHLKS 420

Db 361 CTKVMTDDFLTAHEMGIHQYDMAYAAQPFLLRNGANEFGHEAVGIMSLSATPKHLKS 420

QY 421 IGLLSPDQEDNETEINFLLKQALTIIVGTLPFTYMLEKWRMMVFKGEIPKQDMKKWEM 480

Db 421 IGLLSPDQEDNETEINFLLKQALTIIVGTLPFTYMLEKWRMMVFKGEIPKQDMKKWEM 480

QY 481 KKEIVGVVEPVDHETCDPASLPHVNDYSFIRYTTTLYQFOFQALCOAAKHGEPH 540  
 Db 481 KKEIVGVVEPVDHETCDPASLPHVNDYSFIRYTTTLYQFOFQALCOAAKHGEPH 540  
 QY 541 KDISNSTEAGOKLPMRLKSEPTWLTALENVVGAKNMVRPLNTFELFTWLKDQNK 600  
 Db 541 KDISNSTEAGOKLPMRLKSEPTWLTALENVVGAKNMVRPLNTFELFTWLKDQNK 600  
 QY 601 NSFVGSWSTWSPYADQSKVIRLSKLSALGDKAYEWNDNEMYLPRSSVAYAMROVFLKVKX 660  
 Db 601 NSFVGSWSTWSPYADQSKVIRLSKLSALGDKAYEWNDNEMYLPRSSVAYAMROVFLKVKX 660  
 QY 661 QMILFGEEDVRVANLKPRISNFFVTAPKNVSDIIPRTEVEKALRMGRSINDAFLNDN 720  
 Db 661 QMILFGEEDVRVANLKPRISNFFVTAPKNVSDIIPRTEVEKALRMGRSINDAFLNDN 720  
 QY 721 SLEFLIGIQTLPNPPQPVSIWLVFVGMVGIWVGVILIFTGIRDKKKKARGSENP 780  
 Db 721 SLEFLIGIQTLPNPPQPVSIWLVFVGMVGIWVGVILIFTGIRDKKKKARGSENP 780  
 QY 781 YASIDISKGNPNPQNTDDVQTSF 805  
 Db 781 YASIDISKGNPNPQNTDDVQTSF 805

RESULT 7  
 AAU99701  
 ID AAU99701 standard; Protein; 805 AA.  
 XX  
 AC AAU99701;  
 XX  
 DT 24-SEP-2002 (first entry)  
 XX  
 DE Human angiotensin converting enzyme-2 (ACE-2) protein.  
 XX  
 KW Human; angiotensin converting enzyme-2; ACE-2; body weight disorder;  
 KW muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss;  
 KW lipid metabolism; weight gain; anorexia; cachexia; bulimia; sepsis;  
 KW familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia;  
 KW aberrant metabolic rate; heart failure; left ventricular hypertrophy;  
 KW neurodegenerative disorder; peptide hormone; cytokine processing;  
 KW myocardial infarction; cardiomyopathy; inflammatory bowel disease;  
 KW systemic inflammation response syndrome; polytrauma; pain; stroke;  
 KW bone destruction; rheumatoid arthritis; osteoarthritis; asthma;  
 KW periodontal disease; dysmenorrhoea; premature labour; brain oedema;  
 KW focal injury; diffuse axonal injury; reperfusion injury; scar formation;  
 KW cerebral vasospasm; subarachnoid haemorrhage; allergic disorder;  
 KW adult respiratory distress syndrome; wound healing; appetite;  
 KW body mass index.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Location/Qualifiers  
 FT Peptide  
 FT 1..19  
 FT /label= Signal\_peptide  
 FT Protein  
 FT 19..805  
 FT /label= Mature\_human\_ACE\_2\_protein  
 XX  
 PN WO200239997-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 31-OCT-2001; 2001WO-US45703.  
 XX  
 PR 01-NOV-2000; 2000US-0704216.  
 PR 29-MAY-2001; 2001US-0870382.  
 PR 19-OCT-2001; 2001US-371741P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Acton SL, Ocain TD, Gould AE, Dales NA, Guan B, Brown JA;  
 PI Patane M, Kadambi VU, Solomon M, Stricker-Krongrad A;  
 XX

DR WPI; 2002-547572/58.  
 DR N-PSDB; ABK87623.  
 XX  
 PT Treating body weight disorder and increasing muscle mass comprises  
 PT administering angiotensin converting enzyme-2 modulating compound -  
 XX  
 PS Example 5; Page 387-390; 395pp; English.  
 XX  
 CC The present invention describes a new method of treating a body weight  
 CC disorder, increasing muscle mass and decreasing body fat by  
 CC administration of angiotensin converting enzyme (ACE)-2 modulating  
 CC compound. The invention can be used for treating body weight disorders,  
 CC particularly obesity of at least grade 1, diabetes, atherosclerosis and  
 CC a state associated with lipid metabolism. The method is used for treating  
 CC rapid weight loss, rapid weight gain, anorexia, cachexia, bulimia,  
 CC generalised partial lipodystrophy, familial partial lipodystrophy,  
 CC hypercholesterolaemia, hyperlipidaemia, an aberrant metabolic rate,  
 CC congestive heart failure, chronic heart failure, left ventricular  
 CC hypertrophy, acute heart failure, neurodegenerative disorders (e.g.  
 CC Alzheimer's disease, Parkinson's disease and Huntington's disease),  
 CC diseases associated with peptide hormones or cytokine processing,  
 CC myocardial infarction, cardiomyopathy, systemic inflammation response  
 CC syndrome, sepsis, polytrauma, inflammatory bowel disease, acute and  
 CC chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis  
 CC and periodontal disease, dysmenorrhoea, premature labour, brain oedema  
 CC following focal injury, diffuse axonal injury, stroke, reperfusion  
 CC injury, cerebral vasospasm after subarachnoid haemorrhage, allergic  
 CC disorders including asthma, adult respiratory distress syndrome, wound  
 CC healing and scar formation. The invention decreases the appetite,  
 CC increases muscle mass and decreases body fat of subject having body mass  
 CC index of greater than 23 (preferably 24.9kg/m<sup>2</sup>. The present amino  
 CC acid sequence represents the human ACE-2 protein of the invention.  
 XX  
 SQ Sequence 805 AA;  
 Query Match 100.0%; Score 4291; DB 23; Length 805;  
 Sest Local Similarity 100.0%; Pred. No. 0;  
 Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSSSSLLLSLVATAAQAQSTIEQAKTFLDKFNHEADLFYQSSLSAMWNTNTEENVQ 60  
 Db 1 MSSSSLLLSLVATAAQAQSTIEQAKTFLDKFNHEADLFYQSSLSAMWNTNTEENVQ 60  
 QY 61 NNNNAGDKWAFLEKQSTLAQMPLOEIQNLTKVQLQALQNGSSVLSSEKRLNTIL 120  
 Db 61 NNNNAGDKWAFLEKQSTLAQMPLOEIQNLTKVQLQALQNGSSVLSSEKRLNTIL 120  
 QY 121 NTMTIYSTGKVCNPNPQSCILLRPLNEIMANSLDYNERLWAMESWSEVKGQLRPLY 180  
 Db 121 NTMTIYSTGKVCNPNPQSCILLRPLNEIMANSLDYNERLWAMESWSEVKGQLRPLY 180  
 QY 181 EYVVLKNEMARANHYEDYDGYWRGVDYVNGVDYSGQLIEDVEHTFEIKPLYEHL 240  
 Db 181 EYVVLKNEMARANHYEDYDGYWRGVDYVNGVDYSGQLIEDVEHTFEIKPLYEHL 240  
 QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLGLDMWGFNTNLSLTVPPQCKNIDVTDAMVDQ 300  
 Db 241 HAYVRAKLMNAYPSYISPIGCLPAHLGLDMWGFNTNLSLTVPPQCKNIDVTDAMVDQ 300  
 QY 301 AWDAQRIFKEAEKFFVSGLPNMTQGFWNSMLTDPGNVQKAVCHPTANDLKGDFRILM 360  
 Db 301 AWDAQRIFKEAEKFFVSGLPNMTQGFWNSMLTDPGNVQKAVCHPTANDLKGDFRILM 360  
 QY 361 CTKYTMDDFLTATHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGIMSLSAATPKHLKS 420  
 Db 361 CTKYTMDDFLTATHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGIMSLSAATPKHLKS 420  
 QY 421 IGLLSPDFQEDNETEINFLKQALTVGTLPFTYMLEKRWVMVFKEIIPKQDMKKWEM 480  
 Db 421 IGLLSPDFQEDNETEINFLKQALTVGTLPFTYMLEKRWVMVFKEIIPKQDMKKWEM 480  
 QY 481 KREIVGVVEPVDHETCDPASLPHVNDYSFIRYTTTLYQFOFQALCOAAKHGEPH 540

Db 481 KREIVGVVEPVPHDETYCDPASLFHVSNDSYFIRYTRTYLQFQOEALCOAAKHGEP 540  
 Qy 541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNNVRLPLNYFEPLFTWLKQNK 600  
 Db 541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNNVRLPLNYFEPLFTWLKQNK 600  
 Qy 601 NSFVGMSTWSPYADQSIKVRISLKSALGDKAYEWDNEMYLFRSSVAYAMQYFLKVK 660  
 Db 601 NSFVGMSTWSPYADQSIKVRISLKSALGDKAYEWDNEMYLFRSSVAYAMQYFLKVK 660  
 Qy 661 QMILFGEEDVRVANLKRISFNFTAPKNVSDIIPRTEVEKAIKMSRINDAFRLND 720  
 Db 661 QMILFGEEDVRVANLKRISFNFTAPKNVSDIIPRTEVEKAIKMSRINDAFRLND 720  
 Qy 721 SLEFLGIQFTLGPNNQPPVSIWLVFGVMGVIVGVIVILFTGIRDRKKNKARSGENP 780  
 Db 721 SLEFLGIQFTLGPNNQPPVSIWLVFGVMGVIVGVIVILFTGIRDRKKNKARSGENP 780  
 Qy 781 YASIDISKGENPGFQNTDDVQTSF 805  
 Db 781 YASIDISKGENPGFQNTDDVQTSF 805

RESULT 8  
 AAE20353  
 ID AAE20353 standard; Protein; 805 AA.  
 XX  
 AC AAE20353;  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Human ACE-2 full-length protein.  
 XX  
 KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;  
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;  
 KW myocardial infarction; heart failure; arrhythmia; renal failure; gene;  
 KW inflammation; fertility; enzyme; EC 3.4.15.1.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label= Signal\_peptide  
 FT Protein 19..805  
 FT /note= "Mature ACE-2 protein"  
 FT Domain 19..740  
 FT /note= "Extracellular domain"  
 FT 374..378  
 FT /note= "Zinc binding domain (ZBD)"  
 FT Domain 741..765  
 FT /note= "Transmembrane domain"  
 FT Domain 766..805  
 FT /note= "Cytoplasmic domain"  
 XX  
 PN WO200212471-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 09-AUG-2001; 2001WO-US25059.  
 XX  
 PR 09-AUG-2000; 2000US-0635501.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Acton S, Robison KE, Hsieh FY;  
 XX  
 DR WPI; 2002-257481/30.  
 DR N-PSDB; AAD32586.  
 XX  
 PT Isolated human polypeptide, known as angiotensin converting enzyme-2,  
 PT useful for treating or preventing the development of an abnormal blood  
 PT pressure or related diseases, e.g. hypertension, heart failure or  
 PT myocardial infarction -

XX  
 PS Claim 2; Fig 1; 218pp; English.  
 CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)  
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl  
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful  
 CC for treating or preventing the development of abnormal blood pressure  
 CC and diseases or disorders associated with the protein in a subject. The  
 CC diseases include hypertension, hypotension, congestive heart failure,  
 CC chronic heart failure, acute heart failure, myocardial infarction,  
 CC atherosclerosis, arrhythmia and renal failure. They are also useful  
 CC for treating inflammatory conditions and diseases relating to fertility.  
 CC The present sequence is human full-length ACE-2 protein.  
 XX  
 SQ Sequence 805 AA;  
 Query Match 100.0%; Score 4291; DB 23; Length 805;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSSSSWLLLSLVAVTAAQSTIEBOAKTFLDKFHEADLFYQSSLASWYNNITENVQ 60  
 Db 1 MSSSSWLLLSLVAVTAAQSTIEBOAKTFLDKFHEADLFYQSSLASWYNNITENVQ 60  
 Qy 61 NNNNAGDKWSAFLKEQSTLAQMYPLQEIQLTVKLQALQONGSSVLSEDKSKRLNTIL 120  
 Db 61 NNNNAGDKWSAFLKEQSTLAQMYPLQEIQLTVKLQALQONGSSVLSEDKSKRLNTIL 120  
 Qy 121 NTMSTIYSTGKVCNPNPQECCLLEPGLNEIMANSIDYNERLWAWESWSEVQKQLRPLY 180  
 Db 121 NTMSTIYSTGKVCNPNPQECCLLEPGLNEIMANSIDYNERLWAWESWSEVQKQLRPLY 180  
 Qy 181 EYVVVLKNEMARANHYEDYDYNRGDYEYVNGVDYDYSRQGLIEDVEHTFEIKPLYEHL 240  
 Db 181 EYVVVLKNEMARANHYEDYDYNRGDYEYVNGVDYDYSRQGLIEDVEHTFEIKPLYEHL 240  
 Qy 241 HAYVRAKLNAYPSYISPIGCLPAHLGDMWGFNTNLYSLTVPRGKKNIDVTDAMVQ 300  
 Db 241 HAYVRAKLNAYPSYISPIGCLPAHLGDMWGFNTNLYSLTVPRGKKNIDVTDAMVQ 300  
 Qy 301 AWDAQRIKFEAEKFFSVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDGLKGFRIIM 360  
 Db 301 AWDAQRIKFEAEKFFSVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDGLKGFRIIM 360  
 Qy 361 CTKVTMDDFLTAHEMGHIQYDMAVAAQPFLLRNGANEGFHEAVGIMSLSAATPKHLKS 420  
 Db 361 CTKVTMDDFLTAHEMGHIQYDMAVAAQPFLLRNGANEGFHEAVGIMSLSAATPKHLKS 420  
 Qy 421 IGLSPDFQEDNETEINFLKQALTIIVGTLPFTYMLEKRWMMVFKGEIPKXOMKKWEM 480  
 Db 421 IGLSPDFQEDNETEINFLKQALTIIVGTLPFTYMLEKRWMMVFKGEIPKXOMKKWEM 480  
 Qy 481 KREIVGVVEPVPHDETYCDPASLFHVSNDSYFIRYTRTYLQFQOEALCOAAKHGEP 540  
 Db 481 KREIVGVVEPVPHDETYCDPASLFHVSNDSYFIRYTRTYLQFQOEALCOAAKHGEP 540  
 Qy 541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNNVRLPLNYFEPLFTWLKQNK 600  
 Db 541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNNVRLPLNYFEPLFTWLKQNK 600  
 Qy 601 NSFVGMSTWSPYADQSIKVRISLKSALGDKAYEWDNEMYLFRSSVAYAMQYFLKVK 660  
 Db 601 NSFVGMSTWSPYADQSIKVRISLKSALGDKAYEWDNEMYLFRSSVAYAMQYFLKVK 660  
 Qy 661 QMILFGEEDVRVANLKRISFNFTAPKNVSDIIPRTEVEKAIKMSRINDAFRLND 720  
 Db 661 QMILFGEEDVRVANLKRISFNFTAPKNVSDIIPRTEVEKAIKMSRINDAFRLND 720  
 Qy 721 SLEFLGIQFTLGPNNQPPVSIWLVFGVMGVIVGVIVILFTGIRDRKKNKARSGENP 780  
 Db 721 SLEFLGIQFTLGPNNQPPVSIWLVFGVMGVIVGVIVILFTGIRDRKKNKARSGENP 780  
 Qy 781 YASIDISKGENPGFQNTDDVQTSF 805



KW antinemic; immunosuppressive; cerebroprotective; antimicrobial;  
 KW antiinflammatory; antibacterial; antiparasitic; thyromimetic;  
 KW immunomodulator; antiseborrheic; dermatological; vasoconstriction;  
 KW gastrointestinal disorder; cardiovascular disorder; hypertension;  
 KW coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;  
 KW cachexia; male infertility; impotence; testicular cancer; lung tumor;  
 KW hyperproliferative disorder; pulmonary system disorder;  
 KW central nervous system disorder; bone disorder;  
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; schizophrenia; mania; dementia; paranoia;  
 KW panic disorder; learning disability; anyotropic lateral sclerosis;  
 KW psychoses; autism; sleep disorder; immune system disorder;  
 KW Hashimoto's thyroiditis; musculo-skeletal system disorders;  
 KW multiple sclerosis; ischemic brain injury; stroke; infectious disease;  
 KW diabetes mellitus; immunological disorder; asthma; AIDS; immunogen;  
 KW acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;  
 KW inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;  
 KW neural system disorder; respiratory disorder; olfactory disorder;  
 KW wound healing; chromosome X.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..691  
 FT /label= Extracellular\_domain  
 FT Region 48..55  
 FT /label= Immunogenic\_epitope  
 FT Region 110..118  
 FT /label= Immunogenic\_epitope  
 FT Region 136..146  
 FT /label= Immunogenic\_epitope  
 FT Region 151..158  
 FT /label= Immunogenic\_epitope  
 FT Misc-difference 219  
 FT /label= OTHER  
 FT /note= "Other= Any amino acid encoded by WST"  
 FT Misc-difference 240  
 FT /label= OTHER  
 FT /note= "Other= Any amino acid encoded by RCC"  
 FT Misc-difference 499  
 FT /label= OTHER  
 FT /note= "Other= Any amino acid encoded by NTT"  
 FT Domain 682..698  
 FT /label= Transmembrane\_domain  
 FT  
 XX WO200174896-A1.  
 XX  
 XX 11-OCT-2001.  
 XX  
 XX 02-APR-2001; 2001WO-US10542.  
 XX  
 XX 03-APR-2000; 2000US-194118P.  
 XX 29-SEP-2000; 2000US-2336384P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Moore PA, Mi J, Soppet DR, Coleman TA, Gentz RL, Endress GA;  
 XX Li Y, Dillon RJ;  
 XX  
 XX WPT; 2001-626394/72.  
 XX N-PSDB; AAS14880.  
 XX  
 XX New human proteins, useful for diagnosing, treating, preventing and/or  
 XX prognosing disorders related to the proteins, including cardiovascular  
 XX disorders, autoimmune disorders and reproductive disorders -  
 XX  
 XX Claim 11; Page 298-301; 318pp; English.  
 XX  
 XX The invention relates to novel human proteins (NHP) and the  
 XX nucleic acids that encode them and antibodies raised against them.  
 XX The proteins, antibodies and nucleic acids are useful in the diagnosis,  
 XX prognosis, prevention and/or treatment of diseases and/or disorders  
 XX involving vasoconstriction, gastrointestinal disorders, cardiovascular

CC disorders (e.g. hypertension, erectile dysfunction, high blood pressure,  
 CC coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia,  
 CC cachexia, disorders of small intestine, disorders of reproductive system  
 CC (e.g. male infertility and/or impotence), testicular cancer, lung tumours  
 CC and other hyperproliferative disorders, disorders of pulmonary system,  
 CC central nervous system disorders, bone disorders, neurodegenerative  
 CC diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's  
 CC disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,  
 CC panic disorder, learning disabilities, anyotropic lateral sclerosis,  
 CC psychoses, autism, sleep disorders), immune system disorders (e.g.  
 CC Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,  
 CC central nervous system disorders (e.g. multiple sclerosis, ischemic  
 CC brain injury and/or stroke), infectious diseases, diabetes mellitus,  
 CC immunological disorders (e.g. asthma, acquired immunodeficient syndrome  
 CC (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,  
 CC sepsis, acne, psoriasis and lupus erythematosus), neural system  
 CC disorders, respiratory disorders, olfactory disorders and wound  
 CC healing. The present sequence represents an NHP of the invention the  
 CC gene for which is located on the X chromosome.  
 XX  
 SQ Sequence 711 AA;  
 Query Match 88.0%; Score 3775; DB 22; Length 711;  
 Best Local Similarity 99.3%; Pred. No. 1.5e-311;  
 Matches 704; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 62 MNAGDKWSAFLEKQSTLAQWYPLQETQNLTVKLQALQOQSSVLSSEKSKRLNTILN 121  
 DB 1 MNAGDKWSAFLEKQSTLAQWYPLQETQNLTVKLQALQOQSSVLSSEKSKRLNTILN 60  
 QY 122 TMTSTYTGKVCNPNPQBCLLLEPGLNEITMANSNDYNERLWAWSRSEVGKQRLPYE 181  
 DB 61 TMTSTYTGKVCNPNPQBCLLLEPGLNEITMANSNDYNERLWAWSRSEVGKQRLPYE 120  
 QY 182 EYVVLKNEARANHVEDYDYGWGDYEVNGVDGYDSRGQLEDVEHTEFEIKPYEHLH 241  
 DB 121 EYVVLKNEARANHVEDYDYGWGDYEVNGVDGYDSRGQLEDVEHTEFEIKPYEHLH 180  
 QY 242 AYVPAKLNNAYPSYISPIGCLPAHLIGDMWGRFTWNLVSLTVPFQCKENIDVTAMVQA 301  
 DB 181 AYVPAKLNNAYPSYISPIGCLPAHLIGDMWGRFTWNLVSLTVPFQCKENIDVTAMVQA 240  
 QY 302 WDAQRIPEAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLKGDFFILMC 361  
 DB 241 WDAQRIPEAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLKGDFFILMC 300  
 QY 362 TKVTWDDFLTAHHEMGIQYDMAYAAQPFLLRNGANEGFHEAVGTMSLSAATPKHLSI 421  
 DB 301 TKVTWDDFLTAHHEMGIQYDMAYAAQPFLLRNGANEGFHEAVGTMSLSAATPKHLSI 360  
 QY 422 GLLSPDFQEDNETEINFLKQALTIVGTLPFTYMLEKRWMMVFKEIPKQDQMKQWENK 481  
 DB 361 GLLSPDFQEDNETEINFLKQALTIVGTLPFTYMLEKRWMMVFKEIPKQDQMKQWENK 420  
 QY 482 REIVGVVEVPVPHDETCDPASLFVNDSYFRTYRTLYQFOFQALCOAAKHEGGLHK 541  
 DB 421 REIVGVVEVPVPHDETCDPASLFVNDSYFRTYRTLYQFOFQALCOAAKHEGGLHK 480  
 QY 542 CDISNSTEAGOKLPNMLRLOKSEFWTLALENVVGAQNNVRPLLNYFEPLFTWLKQDNKN 601  
 DB 481 CDISNSTEAGOKLPNMLRLOKSEFWTLALENVVGAQNNVRPLLNYFEPLFTWLKQDNKN 540  
 QY 602 SFVCKWSTDMSPYADQSIKVRISLKSALGDKAVENNDNMYLFRSSVAVAMROYFLKVKQK 661  
 DB 541 SFVCKWSTDMSPYADQSIKVRISLKSALGDKAVENNDNMYLFRSSVAVAMROYFLKVKQK 600  
 QY 662 MILFGEEDVRVANKPRISFNFTAPKQVSDIIPTEVEKEAIRSRSRINDAPFLNDS 721  
 DB 601 MILFGEEDVRVANKPRISFNFTAPKQVSDIIPTEVEKEAIRSRSRINDAPFLNDS 660  
 QY 722 LEFLGIQPTLGPNNQPPVSIWLIVFGVMGVIVGVIVILIFTGIRDRKK 770  
 DB 661 LEFLGIQPTLGPNNQPPVSIWLIVFGVMGVIVGVIVILIFTGIRDRKK 709



## RESULT 11

AA848097  
ID AAB48097 standard; Protein; 805 AA.

XX AC AAB48097;

XX DT 19-MAR-2001 (first entry)

XX DE Mouse Zace2-5 protein.

XX Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;  
KW zinc metalloproteinase; blood pressure; zinc protease; hypertension;  
KW ventricular systolic dysfunction; renal impairment; heart failure;  
KW scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse;  
KW antiarthritic; bradykinin inactivator.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT Region 19..613  
FT /note= "fragment specifically claimed for"  
FT Region 19..708  
FT /note= "fragment specifically claimed for"  
FT Region 19..738  
FT /note= "fragment specifically claimed for"  
FT Region 19..805  
FT /note= "fragment specifically claimed for"  
FT Region 133..542  
FT /note= "fragment specifically claimed for"  
FT Region 344..542  
FT /note= "fragment specifically claimed for"  
FT Region 371..402  
FT /note= "fragment specifically claimed for"

XX WO200070032-A1.

XX PN

XX PD

XX PP

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

CC conditions, including left ventricular systolic dysfunction, progressive  
CC renal impairment, scleroderma renal crisis, congestive heart failure due  
CC to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be  
CC used to treat infertility while Zace2 antagonists are used for inducing  
CC infertility. The present sequence represents the mouse Zace2-5 protein.

XX SQ Sequence 805 AA;

Query Match 83.4%; Score 3579; DB 22; Length 805;

Best Local Similarity 82.1%; Pred. No. 8.3e-295;  
Matches 661; Conservative 60; Mismatches 84; Indels 0; Gaps 0;

QY 1 MSSSSLLSLAVTAATQSTIEQAKTFLDKFNHAEADLFYQSSLSASNNYNTNTEENVQ 60

DB 1 MSSSSLLSLAVTAATQSTIEQAKTFLDKFNHAEADLFYQSSLSASNNYNTNTEENNAQ 60

QY 61 MNMAGDKWAFLEKQSTLAQVPLQEIQLNVLQALQALQNGSSVLSSDKSLRLNTIL 120

DB 61 KMSEAAKWSAFYEQSKTAQSFQEIOTPIKQLQALQNGSSVLSSDKSLRLNTIL 120

QY 121 NTWSTIYSGKVCNPNPOECULLLPGLNEIMANSLDYNRLMWSRSEVQKQLRPLY 180

DB 121 NTWSTIYSGKVCNPNPOECULLLPGLNEIMANSLDYNRLMWSRSEVQKQLRPLY 180

QY 181 EBYVWLKNEARAHYEDYDGYWRGDYEVNGVDYDYSRGOLIEDVETFEIIRPLVEHL 240

DB 181 EBYVWLKNEARAHYEDYDGYWRGDYEVNGVDYDYSRGOLIEDVETFEIIRPLVEHL 240

QY 241 HAYVRKLNAYPSYISPIGCLPAHLGDMGRFTNLYSLTPGQKNDIVTDAMVQ 300

DB 241 HAYVRKLNAYPSYISPIGCLPAHLGDMGRFTNLYSLTPGQKNDIVTDAMVQ 300

QY 301 AWAQRIKFAEAEKFFVSVGLPNNITQGFWENSLMTPDGNVQKAVCHTAMDGLKGFRLIM 360

DB 301 GWAERIFQAEKFFVSVGLPNNITQGFWENSLMTPDGNVQKAVCHTAMDGLKGFRLIM 360

QY 361 CTKVTDDELTAHHENGHIQYDMAYAAQPLRNAGNEGHEAENGLSAAATPKHLKS 420

DB 361 CTKVTDDELTAHHENGHIQYDMAYAAQPLRNAGNEGHEAENGLSAAATPKHLKS 420

QY 421 IGLLSEDFQEDNETEINFLKQALITVGLPTMYLKWNNVFKGEIPKQMKKQWEM 480

DB 421 IGLLSEDFQEDNETEINFLKQALITVGLPTMYLKWNNVFKGEIPKQMKKQWEM 480

QY 481 KREIVGVVPEPHDETYCDPASIFVSNDSYFIRYVYTRTLQYQFQCALCOAKHGLH 540

DB 481 KREIVGVVPEPHDETYCDPASIFVSNDSYFIRYVYTRTLQYQFQCALCOAKHGLH 540

QY 541 KCDISNTEAGQKLFNMLRGKSEPTLALENVGAKNNVRPLNLYPEPLFTWLDQNK 600

DB 541 KCDISNTEAGQKLFNMLRGKSEPTLALENVGAKNNVRPLNLYPEPLFTWLDQNK 600

QY 601 NSFVGMSTWSPVADQSIKVRISLKSALGDKAYENWDMYLFSSVAYAMKQYFLKVK 660

DB 601 NSFVGMSTWSPVADQSIKVRISLKSALGDKAYENWDMYLFSSVAYAMKQYFLKVK 660

QY 661 QMLFGEEDVRVANLKRISFNFFVTPAKVSDIIPRTEVEKAIMSRSRINDAFRLND 720

DB 661 QMLFGEEDVRVANLKRISFNFFVTPAKVSDIIPRTEVEKAIMSRSRINDAFRLND 720

QY 721 SLRFLGIQPTLGPNNOPPVSIWLVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 780

DB 721 SLRFLGIQPTLGPNNOPPVSIWLVGVVGVVGVVGVVGVVGVVGVVGVVGVV 780

QY 781 YASIDTSKGNNGPQNTDDVQTSF 805

DB 781 YDSNDIGKGSNAGFQNSDDAQTSF 805

RESULT 12

ASU07733

ID ABU07733 standard; Protein; 805 AA.

XX



ABU07733;  
 27-MAY-2003 (first entry)  
 Mouse zinc metalloproteinase mZace-5.  
 Mouse; enzyme; mZace-5; zinc metalloproteinase; ulcerative colitis;  
 inflammation; inflammatory bowel disease; arthritis; enterocolitis;  
 Crohn's disease; gene therapy; transgenic.  
 Mus sp.  
 US2002177211-A1.  
 28-NOV-2002.  
 16-OCT-2001; 2001US-0978385.  
 13-MAY-1999; 99US-133952P.  
 27-AUG-1999; 99US-151181P.  
 03-MAY-2000; 2000US-0563516.  
 (ZYMO) ZYMOGENETICS INC.  
 Piddington CS, Petrie C, Shoemaker KE, Bishop PD;  
 WPI; 2003-328489/31.  
 N-PSDB; ABX93335.  
 Isolated human or murine Zace2 polypeptide useful for reducing  
 inflammation in conditions such as inflammatory bowel disease,  
 arthritis, enterocolitis, ulcerative colitis and Crohn's disease -  
 Claim 1; Page 46-48; 57pp; English.  
 The invention relates to an isolated polypeptide, comprising fully  
 defined human Zace2, murine Zace-5, or murine Zace2-10 polypeptide. An  
 expression vector containing Zace2 polynucleotide is useful for producing  
 Zace2 protein. The polynucleotide is useful as a diagnostic probe for  
 detecting a product of Zace2 gene expression in a biological sample. The  
 polypeptide is also useful for decreasing inflammation associated with a  
 condition such as inflammatory bowel disease, arthritis or enterocolitis.  
 The polypeptide is also useful for treating Crohn's disease and  
 ulcerative colitis. The polypeptide is useful for producing labelled  
 angiotensin II, for identifying modulators of zinc protease activity and  
 for identifying angiotensin converting enzyme (ACE) inhibitors. The  
 polynucleotide is useful in gene therapy techniques to treat the above  
 mentioned disorders. The polynucleotide is also useful for determining  
 whether a subject's chromosome contains a mutation in the Zace2 gene. The  
 present sequence represents the amino acid sequence of mouse zinc  
 metalloproteinase mZace-5.  
 Sequence 805 AA;  
 Query Match 83.4%; Score 3579; DB 24; Length 805;  
 Best Local Similarity 82.1%; Pred. No. 8.3e-295;  
 Matches 561; Conservative 60; Mismatches 84; Indels 0; Gaps 0;  
 1 MSSSSWLLLSLVATAQSTIEQAKTFLDKFNHEADLFYQSSLASWYNNYNITEENVQ 60  
 1 MSSSSWLLLSLVAVTTAQSTIEQAKTFLDKFNHEADLFYQSSLASWYNNYNITEENVQ 60  
 61 MNNAAGDWSAFLEQSTLAQMYPLQEIQLNLTQLOALQNGSSVLSDESKRLNITL 120  
 61 KMSEAAKWSAFYEQSKTAQPSLQIQTPIIKRQLQALQSGSSALADKNKQNTIL 120  
 121 NTMSTIYTGKVCNPDNPQECCLLEPGNLNEMANSIDYNRLWAWESWSEVKGQRLPY 180  
 121 NTMSTIYTGKVCNPKNPQECCLLEPGLEIDMATSTDYNRLWAWESWSEVKGQRLPY 180  
 181 EBYVVLKEMARAHYEDYGVWKGDEYVNGVGDYSRQLTJEDVEHTFEIKPLYEHL 240  
 181 EBYVVLKEMARANNYNDYGVWKGDEYVNGVGDYSRQLTJEDVEHTFEIKPLYEHL 240

QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLIGDMWGFNTNLYSLVTPFGCKNIDVTAMWQ 300  
 DB 241 HAYVRAKLMNAYPSYISPIGCLPAHLIGDMWGFNTNLYSLVTPFGCKNIDVTAMWQ 300  
 QY 301 AWDAQRIFKEAEKFFSVGLPNMTQGFWNSMLTDGNVQKAVCHPTAMDLGKGFRIUM 360  
 DB 301 GWAERIFQEAKEKFFSVGLPNMTQGFWNSMLTEPADGRKVVCHPTAMDLGKGFRIUM 360  
 QY 361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPELLNGANEGFHEAVGIMSLSAATPKHLS 420  
 DB 361 CTKVTMDNFLTAAHHEMGHIQYDMAYAAQPELLNGANEGFHEAVGIMSLSAATPKHLS 420  
 QY 421 IGLLSPDFQEDNTEINFLKQALTIIVGTLPTFTYMLEKRWMMVFKGEIPKQOMKQWEM 480  
 DB 421 IGLLSPDFQEDNTEINFLKQALTIIVGTLPTFTYMLEKRWMMVFKGEIPKQOMKQWEM 480  
 QY 481 KREIVGVVEPVPHDETCDPASLPHVNSDYSFYRYTRTYLQFQFQALCOAAKHGPHL 540  
 DB 481 KREIVGVVEPVPHDETCDPASLPHVNSDYSFYRYTRTYLQFQFQALCOAAKHGPHL 540  
 QY 541 KCDISNSTEAGQKLFNMLRGKSEPTWALLENVVGAKMMVRLLNYFPPLFTWLKQNK 600  
 DB 541 KCDISNSTEAGQKLFNMLRGKSEPTWALLENVVGAKMMVRLLNYFPPLFTWLKQNK 600  
 QY 601 NSFVGMSTWSPYADQSIKVRISLKSALGDKAYEMNDNEMFLPRSSVAYAMROYFLKVN 660  
 DB 601 NSFVGMSTWSPYADQSIKVRISLKSALGDKAYEMNDNEMFLPRSSVAYAMROYFLKVN 660  
 QY 661 QMILFGEEDVRVANLKRISFNFTAPKNVSDIIPRTEVEKAIMRSRSHINDAFRLND 720  
 DB 661 QMILFGEEDVRVANLKRISFNFTAPKNVSDIIPRTEVEKAIMRSRSHINDAFRLND 720  
 QY 721 SLEFLGIQTLGPPNPQPVSIWLIIVFGVMGVIVGVIVILIFTGIRDRKKCKKARGENP 780  
 DB 721 SLEFLGIQTLGPPNPQPVSIWLIIVFGVMGVIVGVIVILIFTGIRDRKKCKKARGENP 780  
 QY 781 YASIDISKGNPNQFQNTDVTQSF 805  
 DB 781 YASIDISKGNPNQFQNTDVTQSF 805  
 RESULT 13  
 AAB48098  
 ID AAB48098 standard; Protein; 805 AA.  
 XX AAB48098;  
 AC AAB48098;  
 DX 19-MAR-2001 (first entry)  
 XX Mouse Zace2-10 protein.  
 Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;  
 zinc metalloproteinase; blood pressure; zinc protease; hypertension;  
 ventricular systolic dysfunction; renal impairment; heart failure;  
 scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse;  
 antiarthritic; bradykinin inactivator.  
 Mus sp.  
 Key Location/Qualifiers  
 Region 19..613  
 /note= "fragment specifically claimed for"  
 Region 19..708  
 /note= "fragment specifically claimed for"  
 Region 19..738  
 /note= "fragment specifically claimed for"  
 Region 19..805  
 /note= "fragment specifically claimed for"  
 Region 133..542  
 /note= "fragment specifically claimed for"  
 Region 344..542  
 /note= "fragment specifically claimed for"

FT Region 371..402  
 PT /note= "fragment specifically claimed for"  
 XX WO200070032-A1.  
 XX 23-NOV-2000.  
 XX 03-MAY-2000; 2000WO-US11932.  
 XX 13-MAY-1999; 99US-0311482.  
 XX 27-AUG-1999; 99US-0384706.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Piddington CS, Petrie CR, Shoemaker KE, Bishop PD;  
 XX WPI; 2001-025018/03.  
 XX N-PSDB; AAC84370.  
 XX Angiotensin-converting enzyme, Zace2, useful for treating inflammatory  
 PT bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases  
 PT associated with inflammation such as arthritis and enterocolitis -  
 XX  
 PS Claim 7; Page 113-118; 125pp; English.  
 XX The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-  
 CC converting enzyme is a zinc metalloproteinase that plays roles in blood  
 CC pressure regulation and fertility. Zace2 can be expressed by standard  
 CC recombinant methodology. Zace2 polypeptides are useful for treating an  
 CC inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),  
 CC diseases associated with inflammation like arthritis and enterocolitis,  
 CC as targets for identifying modulators of zinc protease activity, for  
 CC screening or identifying new angiotensin-converting enzyme (ACE)  
 CC inhibitors, and as a basis for rational drug design for inhibitory  
 CC molecules. The nucleic acids can be used to detect the expression of a  
 CC Zace2 gene in a biological sample, as probes for in vivo diagnosis and  
 CC for detecting and localizing Zace2 gene expression in tissue samples,  
 CC to determine whether a subject's chromosomes contain a mutation in the  
 CC Zace2 gene, and to detect aberrations associated with the Zace2 locus.  
 CC Inhibitors of ACE are used for treating hypertension of various  
 CC conditions, including left ventricular systolic dysfunction, progressive  
 CC renal impairment, scleroderma renal crisis, congestive heart failure due  
 CC to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be  
 CC used to treat infertility while Zace2 antagonists are used for inducing  
 CC infertility. The present sequence represents the mouse Zace2-10 protein.  
 XX  
 SQ Sequence 805 AA;  
 Query Match 83.0%; Score 3561; DB 22; Length 805;  
 Best Local Similarity 81.9%; Pred. No. 2.8e-293;  
 Matches 659; Conservative 60; Mismatches 86; Indels 0; Gaps 0;  
 QY 1 MSSSSWLLSLVAVTAAGSTIERAKTFLDKFNHEADLFVQSSLASWYNTNITEENVQ 60  
 DB 1 MSSSSWLLSLVAVTAAGSTIERAKTFLDKFNHEADLFVQSSLASWYNTNITEENAQ 60  
 QY 61 NNNAGDKWSAFLKEQSTLAQYFLOETQNTLVKLOALQONGSSVLSDEKSKRNTIL 120  
 DB 61 KMSEAAKWSAFYEQSQTAFSFLQETQPIIKRQLQALQSSGSSALSADKNQNTIL 120  
 QY 121 NTWSTIYTGKVCNPDNPQECILLEGNTMANSLDYNERLWAWESWRSEVCKQLRPLY 180  
 DB 121 NTWSTIYTGKVCNPDNPQECILLEGNTMANSLDYNERLWAWESWRSEVCKQLRPLY 180  
 QY 181 EYVVLKNEAMRANHYEGDYWRGDYEVNGVDYSGRLTEDVHTFEETKPIYEHL 240  
 DB 181 EYVVLKNEAMRANHYEGDYWRGDYEVNGVDYSGRLTEDVHTFEETKPIYEHL 240  
 QY 241 HAYVRKLMNVPYSIPGICLPAHLGLDMGRFTWNLVSLTPVFGOKPNIIDVTDAMVQ 300  
 DB 241 HAYVRKLMNVPYSIPGICLPAHLGLDMGRFTWNLVSLTPVFGOKPNIIDVTDAMVQ 300  
 QY 301 AWDQRIFKEAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGDFFILM 360

DB 301 GWDARIFKEAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGDFFILM 360  
 QY 361 CTKVTDDELTAHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
 DB 361 CTKVTDDELTAHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
 QY 421 IGLSPDFQEDNTEINFLLKQALTIVGTLPTMYLKKRWNVFKGEIPKQDMKKWHEM 480  
 DB 421 IGLSPDFQEDNTEINFLLKQALTIVGTLPTMYLKKRWNVFKGEIPKQDMKKWHEM 480  
 QY 481 KREIVGVPEVPHDETYCDPASLHVSNDSYFIRYVYTRTLQYQFOEALCOAAKHEGPLH 540  
 DB 481 KREIVGVPEVPHDETYCDPASLHVSNDSYFIRYVYTRTLQYQFOEALCOAAKHEGPLH 540  
 QY 541 KCDISNSTEAGQKLFNMLGKSEBWTALLENVGAKNVRPLNLYPEPLFTWLKQNK 600  
 DB 541 KCDISNSTEAGQKLFNMLGKSEBWTALLENVGAKNVRPLNLYPEPLFTWLKQNK 600  
 QY 601 NSFVGNSTWSPVADOSIKVRLSLKSLGDKAYENNDNEMYLFRSSVAYAMROYFLKVK 660  
 DB 601 NSFVGNSTWSPVADOSIKVRLSLKSLGDKAYENNDNEMYLFRSSVAYAMROYFLKVK 660  
 QY 661 QMLFGEEDVVRVANLKRISFNFFVTAPKQVSDIIPRTEVEKAIKMSRINDAFLINDN 720  
 DB 661 QMLFGEEDVVRVANLKRISFNFFVTAPKQVSDIIPRTEVEKAIKMSRINDAFLINDN 720  
 QY 721 SLFLGIQPTLGPNOPPVSIWLVGVGVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 780  
 DB 721 SLFLGIQPTLGPNOPPVSIWLVGVGVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 780  
 QY 781 YASIDISKGNENFGFQNTDDVQTSF 805  
 DB 781 YASIDISKGNENFGFQNTDDVQTSF 805  
 RESULT 14  
 ABU07734  
 ID ABU07734 standard; Protein; 805 AA.  
 AC ABU07734;  
 XX 27-MAY-2003 (first entry)  
 XX Mouse zinc metalloproteinase mZace-10.  
 XX Mouse; enzyme; mZace-10; zinc metalloproteinase; ulcerative colitis;  
 XX inflammation; inflammatory bowel disease; arthritis; enterocolitis;  
 XX Crohn's disease; gene therapy; transgenic  
 XX Mus sp.  
 XX US2002177211-A1.  
 XX 28-NOV-2002.  
 XX 16-OCT-2001; 2001US-0978385.  
 XX 13-MAY-1999; 99US-133952P.  
 XX 27-AUG-1999; 99US-151181P.  
 XX 03-MAY-2000; 2000US-0563516.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Piddington CS, Petrie C, Shoemaker KE, Bishop PD;  
 XX WPI; 2003-328489/31.  
 XX N-PSDB; ABX93337.  
 XX Isolated human or murine Zace2 polypeptide useful for reducing  
 PT inflammation in conditions such as inflammatory bowel disease,  
 PT arthritis, enterocolitis, ulcerative colitis and Crohn's disease -  
 XX

PS Claim 1; Page 52-54; 57pp; English.

CC The invention relates to an isolated polypeptide, comprising fully  
CC defined human Zace2, murine Zace2-5, or murine Zace2-10 polypeptide. An  
CC expression vector containing Zace2 polynucleotide is useful for producing  
CC Zace2 protein. The polynucleotide is useful as a diagnostic probe for  
CC detecting a product of Zace2 gene expression in a biological sample. The  
CC polypeptide is also useful for decreasing inflammation associated with a  
CC condition such as inflammatory bowel disease, arthritis or enterocolitis.  
CC The polypeptide is also useful for treating Crohn's disease and  
CC ulcerative colitis. The polypeptide is useful for producing labelled  
CC angiotensin II, for identifying modulators of zinc protease activity and  
CC for identifying angiotensin converting enzyme (ACE) inhibitors. The  
CC polynucleotide is useful in gene therapy techniques to treat the above  
CC mentioned disorders. The polynucleotide is also useful for determining  
CC whether a subject's chromosome contains a mutation in the Zace2 gene. The  
CC present sequence represents the amino acid sequence of mouse zinc  
CC metalloproteinase mZace-10.

SQ Sequence 805 AA;

Query Match 83.08; Score 3561; DB 24; Length 805;

Best Local Similarity 81.99; Pred. No. 2.8e-293;

Matches 659; Conservative 60; Mismatches 86; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSVAVTAAGSTIEQAKTFDKFNHEADLFYQSSLSASWNYNTNTEENVQ 60  
 RP 1 MSSSSWLLLSVAVTAAGSTIEQAKTFDKFNHEADLFYQSSLSASWNYNTNTEENNAQ 60  
 QY 61 NNNVAGDKWSAFLEQSTFLAQMPLOEIQNTLVKQLQALQONGSSVLSEDKSKRLNTIL 120  
 DB 61 KXSEAAAKWSAFYEQSKTAQSPSLQEIQTPIKRLQALQONGSSALSADKNQLNTIL 120  
 QY 121 NTMTITISTGKVCNPDNPQCLLEPGLNEIMANSLDYNERLWAWESWRSEVQGKRLPLY 180  
 DB 121 NTMTITISTGKVCNPDNPQCLLEPGLNEIMANSLDYNERLWAWESWRSEVQGKRLPLY 180  
 QY 181 EYVVLKNEMARANHYEDYDYGWGVYGVNGVDYSGQLIEDVETFEIKPLYEHL 240  
 DB 181 EYVVLKNEMARANHYEDYDYGWGVYGVNGVDYSGQLIEDVETFEIKPLYEHL 240  
 QY 241 HAYVRKLMNAPYSYIPICPLPAHLGDMWGFNTNLYSLTFPGQKPNIDVTDAMVQ 300  
 DB 241 HAYVRKLMNAPYSYIPICPLPAHLGDMWGFNTNLYSLTFPGQKPNIDVTDAMVQ 300  
 QY 301 AWDARIFKAEKFFSVGLPNMTQGFWNSMLTDPGVYKAVCHPTAWDLGKGFILM 360  
 DB 301 GMDAERIFQAEKFFSVGLPNMTQGFWNSMLTDPGVYKAVCHPTAWDLGKGFILM 360  
 QY 361 CTKVTMDDFLTAHEMGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
 DB 361 CTKVTMDDFLTAHEMGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
 QY 421 IGLSPQFQDNTEINFLIKQALITVGLTPFTYMLEKRWNVFGEIPKQWKKWEM 480  
 DB 421 IGLSPQFQDNTEINFLIKQALITVGLTPFTYMLEKRWNVFGEIPKQWKKWEM 480  
 QY 481 KREIVGVVPEVPHDETCDPASLFHVSNDYSFIRYTRTYIQFOEALCAAKEGFLH 540  
 DB 481 KREIVGVVPEVPHDETCDPASLFHVSNDYSFIRYTRTYIQFOEALCAAKEGFLH 540  
 QY 541 KCDISNSTEAGOKLFWMLRGKSEPTALENVVGAANNVPLNYPELFTWLKQONK 600  
 DB 541 KCDISNSTEAGOKLFWMLRGKSEPTALENVVGAANNVPLNYPELFTWLKQONK 600  
 QY 601 NSFVGNSTWSPYADQSIKVRISLKGALGANAYEWNDNEMYLFRSSVAYAMQVFLKVN 660  
 DB 601 NSFVGNSTWSPYADQSIKVRISLKGALGANAYEWNDNEMYLFRSSVAYAMQVFLKVN 660  
 QY 661 QMILFGEDVAVALKRIGFNFVTPAKVNSDIIIPRTEVEXAIRMSRSRINDAFRLNDN 720  
 DB 661 QMILFGEDVAVALKRIGFNFVTPAKVNSDIIIPRTEVEXAIRMSRSRINDAFRLNDN 720

QY 721 SLEFLGIQPTLGPBNOPPHYSIMLIVFGVMGVIVLFTGIRDEKKKKNKARSGENP 780  
 DB 721 SLEFLGIQPTLGPBNOPPHYSIMLIVFGVMGVIVLFTGIRDEKKKKNKARSGENP 780  
 QY 781 YASIDISKGNNPGFQNTDDVQTSF 805  
 DB 781 YDSMDIGKGSNAGFQNSDDAQTFSF 805  
 RESULT 15  
 AAU12207  
 ID AAU12207 standard; Protein; 555 AA.  
 XX AC AAU12207;  
 XX DT 24-OCT-2001 (first entry)  
 XX DE Human PRO1885 polypeptide sequence.  
 XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.  
 XX OS Homo sapiens.  
 XX PN WO200140466-A2.  
 XX PD 07-JUN-2001.  
 XX PF 01-DEC-2000; 2000WO-US32678.  
 XX PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99US-030095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30959.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX (GETH) GENENTECH INC.  
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Pilvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 DR WPI; 2001-408281/43.  
 DR N-PSDB; AAS21279.  
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical

XX Claim 12; Fig 72; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane

XX PRO polypeptides. The PRO polypeptides are useful to detect other

XX PRO polypeptides, to link bioactive molecules to cells expressing

XX PRO polypeptides, to modulate biological activities of cells expressing

XX PRO polypeptides, and to detect the presence of mammalian lung, colon,

XX breast, prostate, rectal, cervical or liver tumours by comparing PRO

XX polypeptide expression in a cell sample to that in a control sample.

XX Some of the 275 sequences are also useful to stimulate the release of

XX tumour necrosis factor-alpha (TNF-alpha) from human blood, the

XX proliferation or differentiation of chondrocytes, the proliferation or

XX gene expression in pericyte cells, the release of proteoglycans from

XX cartilage, the proliferation of inner ear utricular supporting cells or

XX of T-lymphocytes, the release of a cytokine from peripheral blood

XX monocytes (PBMCs), or the proliferation of endothelial cells. Some of

XX the PRO polypeptides may modulate glucose or free fatty acid uptake by

XX skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide

XX to factor VIIA. The PRO polypeptides can be used in assays to identify

XX molecules involved in binding interactions. The polynucleotides encoding

XX PRO polypeptides can be used to generate probes, antisense RNA/DNA,

XX transgenic or knock out animals and can be used in gene therapy.

XX SQ Sequence 555 AA;

Query Match 69.4%; Score 2979; DB 22; Length 555;  
Best Local Similarity 99.8%; Pred. No. 4.5e-244;  
Matches 553; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAGSTIEEQAKTFLDKFNHEAEDLFYQSSLSASWNTNTITEENVQ 60  
DB 1 MSSSSWLLLSLVAVTAAGSTIEEQAKTFLDKFNHEAEDLFYQSSLSASWNTNTITEENVQ 60

QY 61 NNNNAGDKWSAPLKEQSTLAQMYPLQEIQNTLVKLQALQONGSSVLSDESKRLNTIL 120  
DB 61 NNNNAGDKWSAPLKEQSTLAQMYPLQEIQNTLVKLQALQONGSSVLSDESKRLNTIL 120

QY 121 NTWSTIYSTGKVCNPDNFECLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180  
QB 121 NTWSTIYSTGKVCNPDNFECLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180

QY 181 EYVVLKNEMARANHYEDYDWRGDYEVNGVDGYDSRGQLIEDVHTFEEIKPLYEHL 240  
DB 181 EYVVLKNEMARANHYEDYDWRGDYEVNGVDGYDSRGQLIEDVHTFEEIKPLYEHL 240

QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMWGRFWTNLYSLTVFPFGQKPNIDVTDAVDQ 300  
DB 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMWGRFWTNLYSLTVFPFGQKPNIDVTDAVDQ 300

QY 301 ANDAQRIKFAEKFFVSGLPNTQGFWENSMLTDRGNQKAVCHPTANDLGKDFRILM 360  
DB 301 ANDAQRIKFAEKFFVSGLPNTQGFWENSMLTDRGNQKAVCHPTANDLGKDFRILM 360

QY 361 CTXVTMDDFLTAHHEMGHIQYDMAAQAQFLLRNGANEGFHEAVGEIMSLSAATPKHLS 420  
DB 361 CTXVTMDDFLTAHHEMGHIQYDMAAQAQFLLRNGANEGFHEAVGEIMSLSAATPKHLS 420

QY 421 IGLSPDFQEDNETEINLLKQALTIVGLTPTVYMLEKRWMMYFKGEIPKQDMKKWEM 480  
DB 421 IGLSPDFQEDNETEINLLKQALTIVGLTPTVYMLEKRWMMYFKGEIPKQDMKKWEM 480

QY 481 KREIVGVVFPVPHDETCDPASLHFVSDYSFIRYTRTLYQFQFQALCQAAKHEGPLH 540  
DB 481 KREIVGVVFPVPHDETCDPASLHFVSDYSFIRYTRTLYQFQFQALCQAAKHEGPLH 540

QY 541 KCDISNSTEAGQKL 554  
DB 541 KCDISNSTEAGQKL 554

Search completed: February 19, 2004, 19:49:43  
Job time : 50 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 19, 2004, 19:48:48 ; Search time 21 Seconds  
(without alignments)  
1621.916 Million cell updates/sec

Title: US-09-163-648-2  
Perfect score: 4291  
Sequence: 1 MSSSSWLLSLVAVTAAQST.....ISKGNPGRQNTDDVGTSTF 805

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/5A.COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/5B.COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/5A.COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/5B.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4291	100.0	805	3	US-08-989-299-2
2	1344	31.3	732	1	US-08-481-626-2
3	1344	31.3	732	3	US-08-989-299-4
4	1337	31.2	1306	3	US-08-989-299-7
5	1334	31.1	732	3	US-08-989-299-5
6	1334	31.1	1312	3	US-08-989-299-8
7	1310	30.5	1313	3	US-08-989-299-9
8	1283	29.9	1310	3	US-08-989-299-10
9	1283	29.9	737	3	US-08-989-299-6
10	1090	25.4	615	3	US-08-989-299-11
11	990	23.1	694	3	US-09-440-325A-1
12	990	23.1	694	4	US-09-846-996A-1
13	642.5	15.0	907	3	US-08-989-299-12
14	376	8.8	212	4	US-09-996-243-387
15	131	3.1	615	4	US-09-107-532A-6507
16	124	2.9	990	2	US-08-645-192B-15
17	120	2.8	990	2	US-08-392-625-20
18	120	2.8	990	2	US-08-466-961A-20
19	118	2.7	3878	4	US-09-914-259-11
20	116.5	2.7	683	3	US-08-630-916A-46
21	115.5	2.7	2008	4	US-09-091-501B-8
22	115.5	2.7	3433	4	US-09-091-501B-10
23	113.5	2.6	665	3	US-08-844-059-2
24	113.5	2.6	665	3	US-09-431-202-2
25	109.5	2.5	499	4	US-09-107-532A-5524
26	109	2.5	686	4	US-09-328-352-4303
27	104	2.4	834	1	US-08-491-357-2

28	104	2.4	834	3	US-08-968-633-2	Sequence 2, Appli
29	104	2.4	834	3	US-09-195-465-2	Sequence 2, Appli
30	104	2.4	834	5	PCT-US96-10823-2	Sequence 2, Appli
31	102.5	2.4	429	4	US-09-194-468A-45	Sequence 45, Appli
32	102.5	2.4	631	3	US-08-448-489-17	Sequence 17, Appli
33	102.5	2.4	660	3	US-08-704-711A-18	Sequence 18, Appli
34	102.5	2.4	660	4	US-09-521-220-18	Sequence 18, Appli
35	102.5	2.4	660	4	US-09-391-104-19	Sequence 19, Appli
36	102	2.4	3169	4	US-09-453-702B-257	Sequence 257, App
37	101.5	2.4	450	3	US-09-306-593-13	Sequence 13, Appli
38	101.5	2.4	560	4	US-09-134-001C-3153	Sequence 3153, Ap
39	101	2.4	984	4	US-09-328-352-6926	Sequence 6926, Ap
40	101	2.4	984	4	US-09-198-452A-841	Sequence 841, App
41	100	2.3	674	4	US-09-107-532A-6201	Sequence 6201, Ap
42	99.5	2.3	789	4	US-09-002-285-84	Sequence 84, Appli
43	99.5	2.3	789	4	US-09-589-477-84	Sequence 84, Appli
44	99.5	2.3	930	4	US-08-953-040-2	Sequence 2, Appli
45	99	2.3	800	4	US-09-107-532A-4095	Sequence 4095, Ap

## ALIGNMENTS

RESULT 1  
US-08-989-299-2  
; Sequence 2, Application US/08989299  
; Patent No. 6194556  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG  
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,299  
; FILING DATE: 11-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold E. Beth  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MIA-025.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 805 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-989-299-2

Query Match 100.0%; Score 4291; DB 3; Length 805;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLSLVAVTAAQSTIEQAKTFLDKFNHEADLFYQSSIASNNYNTNTEENVQ 60  
Db 1 MSSSSWLLSLVAVTAAQSTIEQAKTFLDKFNHEADLFYQSSIASNNYNTNTEENVQ 60  
QY 61 NNNNAGDKWSAFLEKQSTLAQMPLEQNTLVKLQALQNGSSVLSEDKSKRELATIL 120

Db 61 NNNAGDKWSAFLKEQSTLAQMYPQEIQLNLTVKLOLQALQNGSSVLSSEKSLRNTIL 120  
QY 121 NTMSTYTGKVCNPNPQECCLLEPGLNEIMANSLDYNRLWAWESWRSEVKGQLRPLY 180  
Db 121 NTMSTYTGKVCNPNPQECCLLEPGLNEIMANSLDYNRLWAWESWRSEVKGQLRPLY 180  
QY 181 EYVVLKNEMARANHYEDYDGYWKGDEYVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL 240  
Db 181 EYVVLKNEMARANHYEDYDGYWKGDEYVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL 240  
QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMWGFMTNLYSLTVPGQKGNIDVTDAMVQ 300  
Db 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMWGFMTNLYSLTVPGQKGNIDVTDAMVQ 300  
QY 301 ANDAQRIFKEAEKFFSVSGVGLPNTQGWENSMITDGNVQKAVCHPTAWDLGKGFILM 360  
Db 301 ANDAQRIFKEAEKFFSVSGVGLPNTQGWENSMITDGNVQKAVCHPTAWDLGKGFILM 360  
QY 361 CTKVMTDDFLTAHEMGGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
Db 361 CTKVMTDDFLTAHEMGGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
QY 421 IGLSPDFQEDNETETEFNPLKQALITVGLTPTMYLKEKRWNVKGEIPKQWKKWEM 480  
Db 421 IGLSPDFQEDNETETEFNPLKQALITVGLTPTMYLKEKRWNVKGEIPKQWKKWEM 480  
QY 481 KREIVGVVEPVPHDETCDPASLPHVNDYSFIRYTRTYLQFQOEALCOAAKHEGPLH 540  
Db 481 KREIVGVVEPVPHDETCDPASLPHVNDYSFIRYTRTYLQFQOEALCOAAKHEGPLH 540  
QY 541 KCDISNSTEAGOKLFNMLRKGSEPTLALENVVGAKNVVRPLNYPELFTWLKQNK 600  
Db 541 KCDISNSTEAGOKLFNMLRKGSEPTLALENVVGAKNVVRPLNYPELFTWLKQNK 600  
QY 601 NSFVGMSTDNFPYADQIKVIRISKALGDKAYENDNEMYLFRSSVAYAMROFLKVK 660  
Db 601 NSFVGMSTDNFPYADQIKVIRISKALGDKAYENDNEMYLFRSSVAYAMROFLKVK 660  
QY 661 QMILFGEEDVAVLKPRIENFPVTPAKVNSDIIPRTEVEKAIEMSRINDAFRLND 720  
Db 661 QMILFGEEDVAVLKPRIENFPVTPAKVNSDIIPRTEVEKAIEMSRINDAFRLND 720  
QY 721 SLEFLGIQPTLGPQPPVSIWLVFGVNGVIVGIVILIFTGIRDRKKKNGKARSNP 780  
Db 721 SLEFLGIQPTLGPQPPVSIWLVFGVNGVIVGIVILIFTGIRDRKKKNGKARSNP 780  
QY 781 YASIDISKGNPPGFQNTDDVQSP 805  
Db 781 YASIDISKGNPPGFQNTDDVQSP 805

RESULT 2  
US-08-481-626-2  
; Sequence 2, Application US/08481626  
; Patent No. 5801040  
; GENERAL INFORMATION:  
; APPLICANT: Soubrier, Florent  
; APPLICANT: Albenc-Gelas, Francois  
; APPLICANT: Hubert, Christine  
; APPLICANT: Corvol, Pierre  
; TITLE OF INVENTION: Nucleic Acid Coding for the Human  
; TITLE OF INVENTION: Testicular Angiotensin Converting Enzyme (ACE) and its  
; TITLE OF INVENTION: Uses, Especially for the In Vitro Screening for this  
; TITLE OF INVENTION: Enzyme in the Organism  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,626  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/656,183  
FILING DATE: 04-MAR-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 89-09062  
FILING DATE: 05-JUL-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 04958-0006-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 732 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-481-626-2

Query Match 31.3%; Score 1344; DB 1; Length 732;  
Best Local Similarity 41.8%; Pred No. 7,1e-120; Mismatches 204; Indels 38; Gaps 10;  
Matches 259; Conservative 119; Mismatches 204; Indels 38; Gaps 10;

QY 15 TAAQS-----TIEQAKTFLDKENHEAEDLFYQSSLSASNTNITIB-----NVQNM 62  
Db 61 TSACSNLVTDAEAKSFVEYDRTSQVWNEYAEANWNTNITITETSKILQKNQIA 120  
QY 63 NNAGDKWSAFLKEQSTLAQMYPQEIQLNLTVKLOLQALQNGSSVLSSEKSLRNTIL 122  
Db 121 NHT-----LKYGQARKPDVNLQNTTIKRIKKVQDLERAAALPAQELEYNKILD 172  
QY 123 MSTYTGKVCNPNPQECCLLEPGLNEIMANSLDYNRLWAWESWRSEVKGQLRPLYE 182  
Db 173 METTYSVATVCHENG--SCLQLEPDLTNVATSKYEDLLWANEGRDKAGRAILOFYFK 230  
QY 183 YVVLKNEMARANHYEDYDGYWKGDEYVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL 242  
Db 231 YVELINQARLNGYVDAGDSWRSMYETPSLE-----QDLERLFOELQVLYNLHA 280  
QY 243 YVRAKLMNAY-PSYISPIGCLPAHLGDMWGFMTNLYSLTVPGQKGNIDVTDAMVQ 301  
Db 281 YVRRALRHRYGAHINLEGPFAHLGDMWGFMTNLYSLTVPGQKGNIDVTDAMVQ 340  
QY 302 WDAQRIFKEAEKFFSVSGVGLPNTQGWENSMITDGNVQKAVCHPTAWDLGKGFILM 360  
Db 341 WTPRRMFKADDFFTSLGLLPVPEEFNWKSMLEKPTDGRVVCASAMFYNGKDFRIKQ 400  
QY 361 CTKVMTDDFLTAHEMGGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420  
Db 401 CTVNLVEDLVVAHEMGGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 460  
QY 421 IGLSPDFQEDNETETEFNPLKQALITVGLTPTMYLKEKRWNVKGEIPKQWKKWEM 480  
Db 461 LNLSSGGS-D-EHDINFLMKALDKIAFPFSLVDQWNRVFDGSIKTENYNGSWSL 519  
QY 481 KREIVGVVEPVPHDETCDPASLPHVNDYSFIRYTRTYLQFQOEALCOAAKHEGPLH 540  
Db 520 RLKYGQLCPVPTQDGFQAKPHIPSSVPIYRYFVSFIQFQOEALCOAAKHEGPLH 579  
QY 541 KCDISNSTEAGOKLFNMLRKGSEPTLALENVVGAKNVVRPLNYPELFTWLKQNK 600

Db 580 KCDIVQSKAQRATAMKLGSPWPPEAMQLITGQPNMSASAMLSYFKPLDMLRTENE 639  
QY 601 --NSFVGW--STDSPYADQS 617  
Db 640 LHGEKLGWPNQNTWTPNSARS 659

## RESULT 3

US-08-989-299-4  
; Sequence 4, Application US/08989299  
; Patent No. 6194556

; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Robinson, Keith E.

; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG  
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR

; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: FOLEY, HOAG & ELIOT LLP  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,299  
; FILING DATE: 11-DEC-1997

; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold E., Beth

; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MIA-025.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-7000  
; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 732 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-989-299-4

Query Match 31.3%; Score 1344; DB 3; Length 732;  
Best Local Similarity 41.8%; Pred. No. 7.1e-120;  
Matches 259; Conservative 119; Mismatches 204; Indels 38; Gaps 10;

QY 15 TAAQS-----TIEQAKTFLDKFNHEAEDLFYQSSLASWNYNTITEE-----NVQNM 62

Db 61 TSAQSNNLVDEAKSVVEYDRTSQVWNEVAEANNNTNITETSKILLQKNMOIA 120

QY 63 NNAGDKWSAFLEQSTLAQMYPLQIQLNVLKQLQALQMGSSVLSDXSRLNTILNT 122

Db 121 NHT-----LKYGTQAKTQVNLQNTTIKRIKKVQDLERAALPAQEEVYNKILLD 172

QY 123 MSTIVSTGVKVPNDPQSCLLLEPLNEIMNSLDYNERLWAMESVRSVKGQRLPYEE 182

Db 173 METTIVSVATVCHPNG--SCLEQLDPLTNVMTSKYEDLLWAMEGRDKAGRAILOFPK 230

QY 183 YVVLKNEMARAHYEDYGVYRGVDYGVNGVDGYSGQLIEDVHTVEHTPEIKPLVEHLHA 242

Db 231 YVELINQAARLNGYVDAGDSWRSVYETPSLE-----QDLERLFOELQFLYNLHA 280

QY 243 YVRAKLMNAY--PSYISPTGCLPAHLGDMGREFWTLNLSLTVFGQKPNIDVTDAMVQQA 301

Db 281 YVRALHRRHYGAQHNLGSPHALLGNMAQTWSNIYDLVVPFPSPASMDTTEAMLKQG 340

QY 302 WDAQRIKFAEKFPVSVGLPNNMTQGWENSMULTDGNVQKAVCHPTAMDLOG--DFRILM 360

Db 341 WTPRMFKEADDDFTSLGLLPVPEFNNKSMLEKPTDGRVVVCHASAWDFYNGKDFRIKQ 400

QY 361 CTKVTMDDFLTAHEMHGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMLSAATPKHLKS 420

Db 401 CTTVNLEDLVVAHEMHGHIQYFMQYKDLFVALREGANPGFHEAIGDVLALSVSTPKHLHS 460

QY 421 IGLLSPDFQEDNETENFLKQALTTVGLPTFTYMLEKRWVRFKGEIPKQWKKWEM 480

Db 461 LNLISSEGGSD--EHDINFLNKMALDKIAPIPSYLVQKRWVFDGSIKENYQEWWSL 519

QY 481 KREIVGVVPEVPHDETYCDPASLFHVSNDYSIRIYRTRLYQFQFQFQFQFQFQFQFQF 540

Db 520 RLKTYQGLCPVPVPTQGDFFGAKFHIPSPVPIRVFVFIQFQFQFQFQFQFQFQFQF 579

QY 541 KCDISNSTEAGQKLFNNMLRLGKSEPTWTLAENNVGAKNNVRLPLNYPEPLFTWLKQNK 600

Db 580 KCDIVQSKAQRATAMKLGSPWPPEAMQLITGQPNMSASAMLSYFKPLDMLRTENE 639

QY 601 --NSFVGW--STDSPYADQS 617  
Db 640 LHGEKLGWPNQNTWTPNSARS 659

## RESULT 4

US-08-989-299-7  
; Sequence 7, Application US/08989299  
; Patent No. 6194556

; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Robinson, Keith E.

; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG  
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR

; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: FOLEY, HOAG & ELIOT LLP  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,299  
; FILING DATE: 11-DEC-1997

; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold E., Beth

; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MIA-025.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1306 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-989-299-7

Query Match 31.2%; Score 1337; DB 3; Length 1306;  
Best Local Similarity 41.7%; Pred. No. 8.8e-119;  
Matches 255; Conservative 118; Mismatches 204; Indels 34; Gaps 9;

QY 20 TIEQAKTFLDKFNHEAEDLFYQSSLASWNYNTITEE-----NVQNMNAGDKWSA 71

Db 644 TDEAEKFEEDYDRSQVWMEYAEANWNTNITTSKILLQKNOJANHT----- 697  
Qy 72 FLKEQSTLAQMYFLOHONLTVKLOQALQOQSSVLSDESKSLNLTNTMTSTYSTGK 131  
Db 698 --LYGTOARKFVNDQNTNITRIIKYQDLEAALPAQLEBYNKILLDMETTSVAT 755  
Qy 132 VCPNDFPQECLELLEPGLNEIMANSIDYNERLWAMESRSEVKGQRLPXYEYVVLKXEMA 191  
Db 756 VCHENG--SCLEPDLTNVMTSRKYEDLLWAMEGMDKAGRAILOFPKPYVELINOAA 813  
Qy 192 RANHYEDYDQWGDYEVNGVDGYDSRQQLIEDVHTFEIKPLZYHLYHAYVRAKLMA 251  
Db 814 RANGYDAGOSWMTETPSLE-----QDLERLFQZQZLYLNLHAYVRAALRH 863  
Qy 252 Y-PSYISPIGCLPAHLGDMGFWNTNLSYLVFPFGQKPNIDVTDAVMDQAWDAQRIFFE 310  
Db 864 YGAQHINLEGIPIAHLGNNWAGTWSNIYDLVVPFSPASMDITTEAMLKQGMTPRMFKE 923  
Qy 311 AEKFFVSGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 369  
Db 924 ADDFTSLGLLPVPEPFNWSKMLEKFTDGREVVCHASAWDFVNGKDFRIKQCTVWLEDL 983  
Qy 370 LTAHEWHCHTOYMAAQAQFLLRNGANSGFHEAVGEIMSLSAATPKHLKSLGLSPDQ 429  
Db 984 VVAHEWHCHTOYMAAQAQFLLRNGANSGFHEAVGEIMSLSAATPKHLKSLGLSPDQ 1043  
Qy 430 EDNTEINFLKQALITVGLTPFTYMLEKRWNNVFKGIPKQDQWKKWMEKREIVGVVE 489  
Db 1044 SD-EHDINFLKQALITVGLTPFTYMLEKRWNNVFKGIPKQDQWKKWMEKREIVGVVE 1102  
Qy 490 PVPDHTYCDPASLHVSNDYSIRYVTRTYQFQFQALCOAAGHGLKCDINSSTE 549  
Db 1103 PVPDHTYCDPASLHVSNDYSIRYVTRTYQFQFQALCOAAGHGLKCDINSSTE 1162  
Qy 550 AGOKLPMRLGKSEPTLALENVGKNNVRLNLYPELFTWLDKQNK--NSFVGM- 606  
Db 1163 AGOKLPMRLGKSEPTLALENVGKNNVRLNLYPELFTWLDKQNK--NSFVGM- 1222  
Qy 607 STDMSVADQS 617  
Db 1223 QYNWTPNSARS 1233

RESULT 5  
US-08-989-299-5  
; Sequence 5, Application US/08989299  
; Patent No. 6194556  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG  
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,299  
; FILING DATE: 11-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold E. Beth  
; REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: MIA-025.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 732 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-989-299-5

Query Match 31.1%; Score 1334; DB 3; Length 732;  
Best Local Similarity 42.6%; Pred. No. 6.5e-119; Indels 18; Gaps 7;  
Matches 255; Conservative 112; Mismatches 213;

Qy 20 TIEQAKTFLDKFNHEDLPYQSSLASWNTNTNITTEENVQNNAGDKWSAFLEKQSTL 79  
Db 69 TDEAKADRFVEEDYDRAQVLLNEVAEANNQYNTNITTEGSKILLEKSTEVSHTLKYGTR 128  
Qy 80 AQMYPLQETQNLTVKLOQALQOQSSVLSDESKSLNLTNTMTSTYSTGKVCNPDNPQ 139  
Db 129 AKTFDVSNFQSSIKRIIKLQNLDRVLPPKELEEVNQLLDMETTSLSNICVTNG-- 186  
Qy 140 ECLLLEPGLNEIMANSIDYNERLWAMESRSEVKGQRLPXYEYVVLKXEMARAHYEDY 199  
Db 187 TCMLEPDLTNVMTSRKYEDLLWAMEGMDKAGRAILOFPKPYVELINOAA 246  
Qy 200 GDNWGDYEVNGVDGYDSRQQLIEDVHTFEIKPLZYHLYHAYVRAKLMAVPS-YISP 258  
Db 247 GDSWRSLYSDNLE-----QDLKLYQELQPLYNLHAYVRSRHRHYGSEYNL 296  
Qy 259 IGCPLPAHLGDMGFWNTNLSYLVFPFGQKPNIDVTDAVMDQAWDAQRIFFEAEKFFVS 318  
Db 297 DGIPIAHLGNNWAGTWSNIYDLVVPFSPASMDITTEAMLKQGMTPRIFKEADNFTSL 356  
Qy 319 GLPNTQGWNSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTWDDFLTAHEWG 377  
Db 357 GLPVPPEFNNWSKMLEKFTDGREVVCHASAWDFVNGKDFRIKQCTVWLEDLVIAHEG 416  
Qy 378 HIQYDMAYAAQFLLRNGANSGFHEAVGEIMSLSAATPKHLKSLGLSPDQFEDNETEIN 437  
Db 417 HIQYFMOYKDLFTVTFREGANFGHEAIGDINLWALSVPKHLYSLNLLSTE-OSGYEYDIN 475  
Qy 438 FLKQALITVGLTPFTYMLEKRWNNVFKGIPKQDQWKKWMEKREIVGVVFPVPHDEY 497  
Db 476 FLKQALITVGLTPFTYMLEKRWNNVFKGIPKQDQWKKWMEKREIVGVVFPVPHDEY 535  
Qy 498 CDPASLHVSNDYSIRYVTRTYQFQFQALCOAAGHGLKCDINSSTEAGOKLPMN 557  
Db 536 FDPGSRFHPANVPVIRVFSFIQFQFHEALCRAAGTGLKCDIYQSKAGKLLADA 595  
Qy 558 LRLGKSEPTLALENVGKNNVRLNLYPELFTWLDKQNK--NSFVGM-STDWSP 612  
Db 596 MKLGSKFPEAKLITQGNMSASAMNYPKPLTEWLTENRRRHGHTLGLWPEYNAP 653

RESULT 6  
US-08-989-299-8  
; Sequence 8, Application US/08989299  
; Patent No. 6194556  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG  
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; CITY: Boston  
; STATE: MA



COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 11-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold E., Beth  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MIA-025.01  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1312 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-989-299-8

Query Match 31.1%; Score 1334; DB 3; Length 1312;  
Best Local Similarity 42.6%; Pred. No. 1.7e-118;  
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

QY 20 TIEQAKTFLDKFNEADLFYQSSLASWNYNTNITEENVQNNAGDKWSAFLEQSTL 79  
DB 649 TDEAKAFVEEDYRTAKVLNWEYAEANWHYNTNIEGSKILLQNKVEVSNHTLKYG 708  
QY 80 AQMPLOEIQNLTVKLOLQALQONGSSVLSEDSKRLNTILNTMTSTIYSTGKVCNPNPQ 139  
DB 709 AKTFVSNFQNSTIKRIIKKQVNDRAVLPPNELEBYNQILLDMETTVSVANVCYTNG-- 766  
QY 140 ECLLEPGLNEIMANSUDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMARAHYEDY 199  
DB 767 TCMLEPDLTNMWAISRKVEELLWAKSWDRKVGRAILPPFPKYVEFSNKIAKNGYTD 826  
QY 200 GDYWRGDYEVNGVDYSGQLIEDVEHTFEIKPLYEHLHAYVRKLMNAYPS-YISP 258  
DB 827 GDSWRSLSYEDNLE-----QDLKLYOELQPLYNLHAYVRRSLHRHYSYINL 876  
QY 259 IGLPAHLGDMGWFNTNLSLTVPEGQKPNIDVTDAMVDQAWDAQRIKFAEKFFVS 318  
DB 877 DGPPIAHLGNMWAQTSNIYDLVAPPSAPNIDATEAMIKQGWTPRIKFAEADNFFTS 936  
QY 319 GLPNNMTQGFENSMILTDGPNVOKAVCHPTAWDLGK-DPRILMCTKVTDMDFLTAHHEMG 377  
DB 937 GLLPVPPFVWNSMLEKPTDGRVVCVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHEMG 996  
QY 378 HIQDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKSGILLSPDQEDNETEIN 437  
DB 997 HIQYFMQYKDLVPTFREGANPGFHEAIGDIMALSVSTPKHLSLNLSTE-GSGYEYDIN 1055  
QY 438 FLKQALITVGLPTFTYMLKRWVWFVKGPIPKQNMKNWENKREIVGVVFPVPHDETY 497  
DB 1056 FLMKWALDKIATIPPSYILTDWRWRVFDGSIKENYQEWWSURLKYQGLCPVPSRQGD 1115  
QY 498 CDPASLPHYSNDYSIRYVYRTLYQFOFQALCOAAKHEGLPKCDISNSTEAGOKLFNM 557  
DB 1116 FDPGSKFHPANVPVVRVFSFIQFQFHEALCRAAGHTGFLHKCDIYQSKAGKLLADA 1175  
QY 558 LRLKGEPTWTLAENVGAKNNVRPLNLYPELFTWLKQNK--NSFVGV-STWSP 612  
DB 1176 MKLGYSKWPFAKMLITQCPNNSAMNNYFKPLTEWLVTEVNRHGETLGNPEYNAP 1233

RESULT 7

US-08-989-299-9  
Sequence 9, Application US/08989299  
Patent No. 6194556  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan L.  
APPLICANT: Robinson, Keith E.  
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG  
AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 11-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold E., Beth  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MIA-025.01  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1313 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-989-299-9

Query Match 30.5%; Score 1310; DB 3; Length 1313;  
Best Local Similarity 42.0%; Pred. No. 3.5e-116;  
Matches 251; Conservative 115; Mismatches 214; Indels 18; Gaps 7;

QY 20 TIEQAKTFLDKFNEADLFYQSSLASWNYNTNITEENVQNNAGDKWSAFLEQSTL 79  
DB 650 TDEAKAFVEEDYRTAKVLNWEYAEANWHYNTNIEGSKILLQNKVEVSNHTLKYG 709  
QY 80 AQMPLOEIQNLTVKLOLQALQONGSSVLSEDSKRLNTILNTMTSTIYSTGKVCNPNPQ 139  
DB 710 AKTFVSNFQNSTIKRIIKKQVNDRAVLPPNELEBYNQILLDMETTVSVANVCYTNG-- 767  
QY 140 ECLLEPGLNEIMANSUDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMARAHYEDY 199  
DB 768 TCMLEPDLTNMWAISRKVEELLWAKSWDRKVGRAILPPFPKYVDFSNKIAKNGYSDA 827  
QY 200 GDYWRGDYEVNGVDYSGQLIEDVEHTFEIKPLYEHLHAYVRKLMNAYPS-YISP 258  
DB 828 GDSWRSLSYEDNLE-----QDLKLYOELQPLYNLHAYVRRSLHRHYSYINL 877  
QY 259 IGLPAHLGDMGWFNTNLSLTVPEGQKPNIDVTDAMVDQAWDAQRIKFAEKFFVS 318  
DB 878 DGPPIAHLGNMWAQTSNIYDLVAPPSAPNIDATEAMIKQGWTPRIKFAEADNFFTS 937  
QY 319 GLPNNMTQGFENSMILTDGPNVOKAVCHPTAWDLGK-DPRILMCTKVTDMDFLTAHHEMG 377  
DB 938 GLLPVPPFVWNSMLEKPTDGRVVCVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHEMG 997  
QY 378 HIQDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKSGILLSPDQEDNETEIN 437  
DB 998 HIQYFMQYKDLVPTFREGANPGFHEAIGDIMALSVSTPKHLSLNLSTE-GSGYEYDIN 1056

QY 438 FLLKQALITVGTLPFTTLMLEKRWMMVKGEIKDQMKMKWEMKREIVGVVPEVPHDET 497  
 Db 1057 FLMDWALDKAPTFPSVLDIDOWRVPDGSITKENYNGEWSLRLKQGLCPVPSRQGD 1116  
 QY 498 CDPSLHVSNDYSFRYTRILYQFOFOALCOAKHGLPKCDISNSTEAGOKLFNM 557  
 Db 1117 PDPSKHFVPAVPIYRIFISFIQOFHEALCRAAGHTGLPKCDIYQSKAGKLLADA 1176  
 QY 558 LRLKSEPTLALENVVGAKNMVRPLNLYFPFLFTWLKDQNK--NSFVGW-STDWSP 612  
 Db 1177 MKLGYSKQWPEAMKIITGQPNNSASAIMYFRPLTEWLVTNRRRHGETLGPSTWTP 1234

## RESULT 8

US-08-989-299-10  
 ; Sequence 10, Application US/08989299  
 ; Patent No. 6194556  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan L.  
 ; APPLICANT: Robinson, Keith E.  
 ; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG  
 ; AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 ; STREET: One Post Office Square  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109-2170

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/989,299  
 FILING DATE: 11-DEC-1997  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arnold E., Beth  
 REGISTRATION NUMBER: 35,430  
 REFERENCE/DOCKET NUMBER: MIA-025.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-832-1000  
 TELEFAX: 617-832-7000  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1310 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLSCULE TYPE: protein

US-08-989-299-10

Query Match 29.9%; Score 1283.5; DB 3; Length 1310;  
 Best Local Similarity 36.8%; Pred. No. 1.2e-113;  
 Matches 275; Conservative 135; Mismatches 262; Indels 75; Gaps 17;  
 QY 7 LLLSLVAVTAQSTII-----EQAKTFLDKFNHEARDLFYQSSLASNNVNTNI 54  
 Db 21 LLLLLRPPPAALTLDPGLPGDFADEAGARLFASSYNSAEQVLFPRSTAASWAHDTNI 80  
 QY 55 TEENVONNAGDKWSAFLEKQSTLAQMYPLOEI-----ONLT---VKLQALQONGSS 106  
 Db 81 TAENARQEE-----EALLSQEFAEWGKAKELYDPVWQNTDPELRIIGAVRTLGPA 135  
 QY 107 VLSEDKSKRLMTINTWTSTYTGKVCNPNFONPOECLELLEPGLNEIMANSLDYNERLWAVE 166  
 Db 136 NLPLAKRQVNSLSNNSQIYSTGKVCFFNKTASCWSLDPDLNILLASSRSYAMLLFAWE 195  
 QY 167 SWRSEVGKQLRPLYEEVWVLKNEAMAHYEDYGRGDYEVNGVDGYDSRQQLIEDV 226

Db 196 GWHNAVGIPLKPLYCEFTALSNBAYRQDGFSDTGAYWRSWYDSPTFE-----EDL 245  
 QY 227 EHTFEIPELPEHLHAYVRAKLANAY--PSYISPIGCLPAHLGLDMWGRFTNLSLTVPF 285  
 Db 246 ERIYQLPEPLYNLAHYVRVLHRRYCDRIYNLRGIPPAHLGNWMAQSWESIYDMVVPF 305  
 QY 286 GQKPNIDVTAMDQDAQRIKFAEKFPVSVGLPNWTCQGFWNSMLTDPGNVQKAVCH 345  
 Db 306 PKPKPLDVTSTWQKGNWATHMFRVAEBEFTSLGLLPMPPFMAESMLEKPEDGSEVVCH 365  
 QY 346 PTAWDL-GRKSDPRILMCTKVTMDDELTAHHEMGHIQYDMAYAAQFPFLNNGANEGFHEAV 404  
 Db 366 ASADFYNRKDFRIKQCTQVTMDOLSTVHHEMGHVQYLQYKQDQPVSLRR-ANPGFHEAI 424  
 QY 405 GRIMISLAATPKHLKSLGLSPDQEDNETEINFLKQALTIIVGLTLPFTYMLEKRWVVF 464  
 Db 425 GDVLSVSTPAHLKIGLLD-HVTNDESDIYNLLKMALEKIAFLPGYLVQDQWGVF 483  
 QY 465 KGEIPKQDQMKWEMKREIVGVVEPVPHDETCDPASLPHVNSDYSPYRITRILYQFO 524  
 Db 484 SORTPSSRYNFDWYLRTKYQICPPVVRNETHFDAGAKPHIPSVTPYIRYFVSFVLOQ 543  
 QY 525 FOEALCOAKHEGLPKCDISNSTEAGOKLFNMLRLKSEPTLALENVVGAKNMVRPL 584  
 Db 544 FHALCMEAGHQGLHQCDIYQSTRAGAKLRAVLQAGCSRPMQEVLDKMWASDALDAQPL 603  
 QY 585 LAYEPLFTWLKDQKNS--FVGW-STDWSPYADQSIKVRISLKSALG-----DKA 632  
 Db 604 LDYFQVTCWLOEQNERNGEVLGWPEYQWRPPLNNYPEGIDLVTDDEASRFEYEDRS 663  
 QY 633 YE--WND-----NEMYLFRSSVAYANRQYFLKVKQOMILFGEEDVRVANLAPRISFNFF 684  
 Db 664 FOAVMNEYAEANWYNTWITTEASKILLQKNMOIANHTLYG-----NWARRFDVSNF 716  
 QY 685 VTAP-----KNVSD---IIPRTEVEK 702  
 Db 717 QNATSKRIIKKQVQLQRAVLVPKELEE 743

## RESULT 9

US-08-989-299-6  
 ; Sequence 6, Application US/08989299  
 ; Patent No. 6194556  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan L.  
 ; APPLICANT: Robinson, Keith E.  
 ; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG  
 ; AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 ; STREET: One Post Office Square  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109-2170  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/989,299  
 ; FILING DATE: 11-DEC-1997  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Arnold E., Beth  
 ; REGISTRATION NUMBER: 35,430  
 ; REFERENCE/DOCKET NUMBER: MIA-025.01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-832-1000  
 ; TELEFAX: 617-832-7000  
 ; INFORMATION FOR SEQ ID NO: 6:



```
RESULT 11
US-09-440-325A-1
; Sequence 1, Application US/09440325A
; Patent No. 6280994
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: 98-79
; CURRENT APPLICATION NUMBER: US/09/440,325A
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(694)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-440-325A-1

Query Match      23.1%; Score 990; DB 3; Length 694;
Best Local Similarity 32.3%; Pred. No. 6.4e-86;
Matches 241; Conservative 121; Mismatches 258; Indels 126; Gaps 22;

QY 22 EQAKTFLDKFHEAEDLFYQSSLASNYNTNITEENVQNNAGDKWSAPLKEQSTLAQ 81
DB 53 ETETKIFLOFYDQTGEVNLKFMETATNTVITRKNQENMKDMER-SQFMIFYGTQAH 111
QY 82 MYPLQEIQNTLVKQLQALQONGSSVLSSEKSKRLNTILNTMTSTIYTGVCNPDNPQEC 141
DB 112 LFKVTFKPDVNGMLSKLQNDKALSKDEIRYNELLAXLEMTYSMAQVCLNEG- C 169
QY 142 LLEPGNEIMANSLDYNRLIWAWSERSEVKGQRLPIYEVVLKNEMARAH- YEDYG 200
DB 170 LSLESEL-EYMATSRDKELLMAWQGDVAGROICTTFFHYVELSKAQLNGVXKDMG 228
QY 201 DYRGDYEVNGVDGYDSRGQIEDVHTFBEIKPLHYHLHAYVRAKLNNAY-PSYISPI 259
DB 229 ALMHSKYESTLE-----QDLERLFQELRPLYNPHYVRRALHRYGPELIDL 278
QY 260 GCLPAHLIGD-MWGRFWNLISLTVPFGOKPNIDVTDAWQDQADQRI-FKEAEKFFVS 317
DB 279 GPIPAHLGENTLAQSNVNLDPVLFKKIPEDVTIKMKVQHWKPEKLMLEAEETFTY 338
QY 318 VG--LPNMTQGFWNSMLTDPGNVQKAVCHPTAMDLGK-GDPRILMCTKVTMDDFLTAHH 374
DB 339 LGLALPAPPSPFWKLMLEMRPTDGREVECHISAWNFYQDDDFRIKKCAEVTTEDPLSIFH 398
QY 375 EMGHIQYDMAAQAQPLLRNGANEGFHEAVGEIMSLSAATPKHLKSIIGLLSPDFQEDNET 434
DB 399 EMGHFQYFLOQYNLSIIFRTGANPAFEAAGSVITLSASSHKLNLIGLLS--LLED--- 453
QY 435 EINFLLKQALTIQVTLPTFTYMLKRWMMVKGEIKDQWKKWEMER-EIVGVVEVPH 493
DB 454 EVNFMHIALEKIAFIPFGIMDLFRKVPDGTGIMDIYQEWNLRLKTKQGLCPAIPH 513
QY 494 DETYCDPASLPHVSNDSYFI-RYYTTLTYQFOQEAALCOAAKHEGLHKDCISNSTBAQ 552
DB 514 SEEDPDPGAKFHFSAGVPIRIRYFLSLVLFQFQFHETLCKASGMGMLHQCDDIYNSKIAG 573
QY 553 KLFNMLRLCKSEPMTLALENVGAKNNVRPLINPEPLFTMLKQDNKNSFVGWSTDWSP 612
DB 574 LL--ALKLSSKPWEVLKMLTGESEVSTNVFTYFKPLLTL----- 614
QY 613 YADQSIKVRISLKGALGDKAYENDNEMLYFRSSVAYANRQYFLKVNQMILFGEEDVRV 672
DB 615 -----VTEHAARGE----- 623
QY 673 ANLKPRISFNFFVTAPXNVSDIIPRTEVEKAIHMSRSRINDAFRLNDNSLFLGIQPTLG 732

US-09-846-996A-1
; Sequence 1, Application US/09846996A
; Patent No. 6524835
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Zacel: A Human Metalloenzyme
; FILE REFERENCE: 98-79D1
; CURRENT APPLICATION NUMBER: US/09/846,996A
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 09/440,325
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/109,783
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (152)...(152)
; OTHER INFORMATION: Xaa is any amino acid.
; NAME/KEY: VARIANT
; LOCATION: (224)...(224)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-846-996A-1

Query Match      23.1%; Score 990; DB 4; Length 694;
Best Local Similarity 32.3%; Pred. No. 6.4e-86;
Matches 241; Conservative 121; Mismatches 258; Indels 126; Gaps 22;

QY 22 EQAKTFLDKFHEAEDLFYQSSLASNYNTNITEENVQNNAGDKWSAPLKEQSTLAQ 81
DB 53 ETETKIFLOFYDQTGEVNLKFMETATNTVITRKNQENMKDMER-SQFMIFYGTQAH 111
QY 82 MYPLQEIQNTLVKQLQALQONGSSVLSSEKSKRLNTILNTMTSTIYTGVCNPDNPQEC 141
DB 112 LFKVTFKPDVNGMLSKLQNDKALSKDEIRYNELLAXLEMTYSMAQVCLNEG- C 169
QY 142 LLEPGNEIMANSLDYNRLIWAWSERSEVKGQRLPIYEVVLKNEMARAH- YEDYG 200
DB 170 LSLESEL-EYMATSRDKELLMAWQGDVAGROICTTFFHYVELSKAQLNGVXKDMG 228
QY 201 DYRGDYEVNGVDGYDSRGQIEDVHTFBEIKPLHYHLHAYVRAKLNNAY-PSYISPI 259
DB 229 ALMHSKYESTLE-----QDLERLFQELRPLYNPHYVRRALHRYGPELIDL 278
QY 260 GCLPAHLIGD-MWGRFWNLISLTVPFGOKPNIDVTDAWQDQADQRI-FKEAEKFFVS 317
DB 279 GPIPAHLGENTLAQSNVNLDPVLFKKIPEDVTIKMKVQHWKPEKLMLEAEETFTY 338
QY 318 VG--LPNMTQGFWNSMLTDPGNVQKAVCHPTAMDLGK-GDPRILMCTKVTMDDFLTAHH 374
DB 339 LGLALPAPPSPFWKLMLEMRPTDGREVECHISAWNFYQDDDFRIKKCAEVTTEDPLSIFH 398
QY 375 EMGHIQYDMAAQAQPLLRNGANEGFHEAVGEIMSLSAATPKHLKSIIGLLSPDFQEDNET 434
DB 399 EMGHFQYFLOQYNLSIIFRTGANPAFEAAGSVITLSASSHKLNLIGLLS--LLED--- 453
QY 435 EINFLLKQALTIQVTLPTFTYMLKRWMMVKGEIKDQWKKWEMER-EIVGVVEVPH 493
DB 454 EVNFMHIALEKIAFIPFGIMDLFRKVPDGTGIMDIYQEWNLRLKTKQGLCPAIPH 513
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QY 494 DETYCDPASLHVNDYSFI-RYVTRTLVQFOEALCOAAXHEGFLKCDISKSTRAGQ 552  
DB 514 SEEDFPOAKHFRAGVPIRIRFLSLVQLQFHEILCKASGHMGLHQCDLYNKKIAGK 573  
QY 553 KLFNMLRGKSEPTWLALENVVGAKNNVRPLNYPFLFTWLKDONKNSFVGMSTWSP 612  
DB 574 LL--ALKLGSCKPMPPEVLKMLTGESEVSTNVFMTYFKPLLTWL----- 614  
QY 613 VADQSIKVRISLKGALGSKAYEMNDNEMYLFRSSVAYAMRQVFLKVNQMLFGSEEDVRV 672  
DB 615 -----VIEHARGE----- 623  
QY 673 ANLKPRISFNFTAPKXVSDIIPRTEVEKALRMSRINDAFRNDNSLEPLGIQPTLG 732  
DB 624 ---TGVPLQFY--PPVET-----PMSSTK-----DTRKVTFLSLK----- 656  
QY 733 PNPQPPVSIW-LIVFGVVMGVIVGI 757  
DB 657 DPNQAKFGYVLLALGFVMSLVVLGL 682

## RESULT 13

US-08-989-299-12  
Sequence 12, Application US/08989299  
Patent No. 6194556  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan L.  
APPLICANT: Robinson, Keith E.  
TITLE OF INVENTION: ANGIOGENIN CONVERTING ENZYME HOMOLOG  
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: FOLEY, HOAG & ELIOT LLP  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/989,299  
FILING DATE: 11-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold E., Beth  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MIA-025.01  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 907 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-989-299-12

Query Match 15.0%; Score 642.5; DB 3; Length 907;  
Best Local Similarity 27.0%; Pred. No. 2, 3e-52;  
Matches 172; Conservative 136; Mismatches 289; Indels 41; Gaps 19;  
QY 2 SSSWLLSLVAVTAQAQSTIEQAKTFLDXFNHEADBLFYQSSLASWNTNTNTEENVQN 61  
DB 160 SSNYKTNLQAGSIKD--BEKLSWLAGYEAIAKVLREVALSVGMRYFNDAFSLKLA 217  
QY 62 MNNAGDKWSAFLEKQSTLAQMPYQEIQNLTVKLQALQOQNGSSVLSDEKSKRLNTILN 121

DB 218 LDEAVNLTPVRSTSMQAKQPDMA SVTDEKVMRQLGVVSPGMSALAPSRFADYSQAQ 277  
QY 122 TMSIITYSTGVKCNPDNPQECGLLEPGLNIMANSLDYNERLWAWESWSEVGVKQLRPLYE 181  
DB 278 ALNRDSKSTICDCKDVPCCALQKIDMSIFRNEKDSRLQHLWVSYVTAIAXS-KPSYN 336  
QY 182 EYVWLKQEMARAHYEDYDYNRGDYEVNG-VGVYDYSRGLIEDVEHTFBEIKPLYEHL 240  
DB 337 NIITISNEGAKLNGFANGAMRSAPFDMSSKVHKAFF---DLNKQIDIKIYSTIQPFYOLL 393  
QY 241 HAYVRAKLMNAY--PSVISPIGCLPAHLGLDMGRENWNLVSLTPFGQKPNIDVTDAMV 298  
DB 394 HAYWRQLAGIYSNPVGLSKDGPAPHLFGSLDGGDSAHYEQTKPFHEES--ETPEAML 451  
QY 299 D-----QAWDAQRIPEKAEKFFVSGLPNVTOGFWNSMLTDPNVQKAVCHP-TANDL-G 352  
DB 452 SAFTQNTYTTKKNFVTAIRYFKSAGFPFLPKSWTSSIFARVWS-KDWICHFAALDMRA 510  
QY 353 KGDFFILMCTKVTMDDELTAHHEMGIQYDMAYAAQPFLLRNGANEGFHEAVGEIMLSA 412  
DB 511 PNDFRVKACAQLGEPDFEQAHSLLVQTYQYLYKQOSLLFREQASPVITDAIANAFHLS 570  
QY 413 ATPKHLKSGILLSPDFQDNETS-INFLKQALTIIVGLTPFTYMLEKRWVVKGEIKPD 471  
DB 571 TNPVLYSOKLVPSEHLDIKDSVILNKLKESLESFTKLPTFIADNWRVYELFDGTVEKN 630  
QY 472 OMKKWEMKREIVGVVPEVPHDRTYCDPASLPH--VSNDSYFIYYTRTL-----YQFQF 525  
DB 631 KINDRWMEIRNKYEGVRSQPYNTSNLD--ALJHNSVQVHS---PATRTLISYVYLKFOI 685  
QY 526 QEALCQAA---KHEGPHLKCDISNSTEAGOKLFNMLRGKSEFPWTLALENVVGAKNNVR 582  
DB 686 LKALCQRELFWLSEG---CILSEDTT--EKLRETKLGGSSITLWLALEMISGKGLDAQ 739  
QY 583 PLINNYFEPLFTWLKQNK--NSFVGKSTOWSPYADQSI 618  
DB 740 PLEETIEPLINWLRNTNEIDQVVVVGDDGEGTPTTVEEI 777

## RESULT 14

US-09-996-243-387  
Sequence 387, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashtenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14

1	PRIOR APPLICATION NUMBER: 60/049787	1	PRIOR FILING DATE: 1998-06-12
2	PRIOR FILING DATE: 1997-06-15	2	PRIOR APPLICATION NUMBER: 60/089444
3	PRIOR APPLICATION NUMBER: 60/062250	3	PRIOR FILING DATE: 1998-06-15
4	PRIOR FILING DATE: 1997-10-17	4	PRIOR APPLICATION NUMBER: 60/089512
5	PRIOR APPLICATION NUMBER: 60/065186	5	PRIOR FILING DATE: 1998-06-16
6	PRIOR FILING DATE: 1997-11-12	6	PRIOR APPLICATION NUMBER: 60/089514
7	PRIOR APPLICATION NUMBER: 60/065311	7	PRIOR FILING DATE: 1998-06-16
8	PRIOR FILING DATE: 1997-11-13	8	PRIOR APPLICATION NUMBER: 60/089532
9	PRIOR APPLICATION NUMBER: 60/066770	9	PRIOR FILING DATE: 1998-06-17
10	PRIOR FILING DATE: 1997-11-24	10	PRIOR APPLICATION NUMBER: 60/089538
11	PRIOR APPLICATION NUMBER: 60/075945	11	PRIOR FILING DATE: 1998-06-17
12	PRIOR FILING DATE: 1998-02-25	12	PRIOR APPLICATION NUMBER: 60/089598
13	PRIOR APPLICATION NUMBER: 60/078910	13	PRIOR FILING DATE: 1998-06-17
14	PRIOR FILING DATE: 1998-03-20	14	PRIOR APPLICATION NUMBER: 60/089599
15	PRIOR APPLICATION NUMBER: 60/083322	15	PRIOR FILING DATE: 1998-06-17
16	PRIOR FILING DATE: 1998-05-28	16	PRIOR APPLICATION NUMBER: 60/089600
17	PRIOR APPLICATION NUMBER: 60/087607	17	PRIOR FILING DATE: 1998-06-17
18	PRIOR FILING DATE: 1998-06-02	18	PRIOR APPLICATION NUMBER: 60/089653
19	PRIOR APPLICATION NUMBER: 60/087609	19	PRIOR FILING DATE: 1998-06-17
20	PRIOR FILING DATE: 1998-06-02	20	PRIOR APPLICATION NUMBER: 60/089801
21	PRIOR APPLICATION NUMBER: 60/087759	21	PRIOR FILING DATE: 1998-06-18
22	PRIOR FILING DATE: 1998-06-02	22	PRIOR APPLICATION NUMBER: 60/089908
23	PRIOR APPLICATION NUMBER: 60/087827	23	PRIOR FILING DATE: 1998-06-18
24	PRIOR FILING DATE: 1998-06-03	24	PRIOR APPLICATION NUMBER: 60/089947
25	PRIOR APPLICATION NUMBER: 60/088021	25	PRIOR FILING DATE: 1998-06-19
26	PRIOR FILING DATE: 1998-06-04	26	PRIOR APPLICATION NUMBER: 60/089948
27	PRIOR APPLICATION NUMBER: 60/088025	27	PRIOR FILING DATE: 1998-06-19
28	PRIOR FILING DATE: 1998-06-04	28	PRIOR APPLICATION NUMBER: 60/089952
29	PRIOR APPLICATION NUMBER: 60/088026	29	PRIOR FILING DATE: 1998-06-19
30	PRIOR FILING DATE: 1998-06-04	30	PRIOR APPLICATION NUMBER: 60/090246
31	PRIOR APPLICATION NUMBER: 60/088028	31	PRIOR FILING DATE: 1998-06-22
32	PRIOR FILING DATE: 1998-06-04	32	PRIOR APPLICATION NUMBER: 60/090252
33	PRIOR APPLICATION NUMBER: 60/088029	33	PRIOR FILING DATE: 1998-06-22
34	PRIOR FILING DATE: 1998-06-04	34	PRIOR APPLICATION NUMBER: 60/090254
35	PRIOR APPLICATION NUMBER: 60/088030	35	PRIOR FILING DATE: 1998-06-22
36	PRIOR FILING DATE: 1998-06-04	36	PRIOR APPLICATION NUMBER: 60/090349
37	PRIOR APPLICATION NUMBER: 60/088033	37	PRIOR FILING DATE: 1998-06-23
38	PRIOR FILING DATE: 1998-06-04	38	PRIOR APPLICATION NUMBER: 60/090355
39	PRIOR APPLICATION NUMBER: 60/088326	39	PRIOR FILING DATE: 1998-06-23
40	PRIOR FILING DATE: 1998-06-04	40	PRIOR APPLICATION NUMBER: 60/090429
41	PRIOR APPLICATION NUMBER: 60/088167	41	PRIOR FILING DATE: 1998-06-24
42	PRIOR FILING DATE: 1998-06-05	42	PRIOR APPLICATION NUMBER: 60/090431
43	PRIOR APPLICATION NUMBER: 60/088202	43	PRIOR FILING DATE: 1998-06-24
44	PRIOR FILING DATE: 1998-06-05	44	PRIOR APPLICATION NUMBER: 60/090435
45	PRIOR APPLICATION NUMBER: 60/088212	45	PRIOR FILING DATE: 1998-06-24
46	PRIOR FILING DATE: 1998-06-05	46	PRIOR APPLICATION NUMBER: 60/090444
47	PRIOR APPLICATION NUMBER: 60/088217	47	PRIOR FILING DATE: 1998-06-24
48	PRIOR FILING DATE: 1998-06-05	48	PRIOR APPLICATION NUMBER: 60/090445
49	PRIOR APPLICATION NUMBER: 60/088655	49	PRIOR FILING DATE: 1998-06-24
50	PRIOR FILING DATE: 1998-06-09	50	PRIOR APPLICATION NUMBER: 60/090472
51	PRIOR APPLICATION NUMBER: 60/088734	51	PRIOR FILING DATE: 1998-06-24
52	PRIOR FILING DATE: 1998-06-10	52	PRIOR APPLICATION NUMBER: 60/090542
53	PRIOR APPLICATION NUMBER: 60/088738	53	PRIOR FILING DATE: 1998-06-24
54	PRIOR FILING DATE: 1998-06-10	54	PRIOR APPLICATION NUMBER: 60/090557
55	PRIOR APPLICATION NUMBER: 60/088742	55	PRIOR FILING DATE: 1998-06-24
56	PRIOR FILING DATE: 1998-06-10	56	PRIOR APPLICATION NUMBER: 60/090576
57	PRIOR APPLICATION NUMBER: 60/088810	57	PRIOR FILING DATE: 1998-06-25
58	PRIOR FILING DATE: 1998-06-10	58	PRIOR APPLICATION NUMBER: 60/090678
59	PRIOR APPLICATION NUMBER: 60/088824	59	PRIOR FILING DATE: 1998-06-25
60	PRIOR FILING DATE: 1998-06-10	60	PRIOR APPLICATION NUMBER: 60/090690
61	PRIOR APPLICATION NUMBER: 60/088826	61	PRIOR FILING DATE: 1998-06-25
62	PRIOR FILING DATE: 1998-06-10	62	PRIOR APPLICATION NUMBER: 60/090894
63	PRIOR APPLICATION NUMBER: 60/088858	63	PRIOR FILING DATE: 1998-06-25
64	PRIOR FILING DATE: 1998-06-11	64	PRIOR APPLICATION NUMBER: 60/090695
65	PRIOR APPLICATION NUMBER: 60/088861	65	PRIOR FILING DATE: 1998-06-25
66	PRIOR FILING DATE: 1998-06-11	66	PRIOR APPLICATION NUMBER: 60/090696
67	PRIOR APPLICATION NUMBER: 60/088876	67	PRIOR FILING DATE: 1998-06-25
68	PRIOR FILING DATE: 1998-06-11	68	PRIOR APPLICATION NUMBER: 60/090699
69	PRIOR APPLICATION NUMBER: 60/089105	6	

PRIOR APPLICATION NUMBER: 60/090862  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 8.8%; Score 376; DB 4; Length 212;  
 Best Local Similarity 47.9%; Pred. No. 8e-28;  
 Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

Qy 612 PVADQSIKVRISLKGALGDYKAYWNDNEMYLFRSSVAYAMQVFLKVNQMLFGESDVR 671  
 Db 19 PGAEAFKVRLLSIRLALGDYKAYWDTNEEYLFKAMVAFNR----KVPREAT-BISHVL 73  
 Qy 672 VAMLKPRISFNFTAPKNVSDIIFRTEVEKAKRMSRSINDAFRLNDNSLEFLGIQPTL 731  
 Db 74 LCNVTQVSEFWFVDTSPK-NHTLPAVEVQSAIRMNKNINNAFFLNDOTLEFLKIPSTL 132  
 Qy 732 GPNQSPVSMILVFGVMGVVGVIVLIFTGIRKXKNKARS 776  
 Db 133 APMPSEVPINILIFGVIFCIIIVAILLILSLGWERRKNKEPS 177

## RESULT 15

US-09-107-532A-6507  
 Sequence 6507, Application US/09107532A  
 Patent No. 6583275  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 City: Waltham  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02354  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-ROM ISO9660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107.532A  
 FILING DATE: 30-Jun-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/085,598  
 FILING DATE: 14 May 1998  
 APPLICATION NUMBER: 60/051571  
 FILING DATE: July 2, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ariniello, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277  
 INFORMATION FOR SEQ ID NO: 6507:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 615 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ORIGINAL SOURCE:  
 ORGANISM: Enterococcus faecium  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (B) LOCATION 1...615  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6507:  
 US-09-107-532A-6507

Query Match 3.1%; Score 131; DB 4; Length 615;  
 Best Local Similarity 20.1%; Pred. No. 0.0016;  
 Matches 127; Conservative 87; Mismatches 227; Indels 190; Gaps 31;  
 Qy 3 SSSWLLSLVAVTAAQSTIEBOAKTFDKFNHBAEDLFYQSSLASWYNTNTNTEENVQNM 62  
 Db 20 SLWNWLDSPFSGSHSDALNQMKQLEDQNMNE-----YYHRTVKNSPSS---DNAEQL 69  
 Qy 63 NNAGDKMSAFLEKEQSTL-----AQMYPLQEQIN 90  
 Db 70 N-----AILQIQETITNGTQSSYITALLSANVNDSDAKVLGKLYAMLPRLQSAET 122  
 Qy 91 L-----TVKLQALQOONGSSVLSEDKSKRLNTI-----LNTM 123  
 Db 123 VLSKKFAEISDNDNQMLSQSSFEITAFRLNEIRDSQSLSEAEENIINTLSLQGLNAW 182  
 Qy 124 STLYST--GKVCNP--DNQECILLPG--LNEIMAN--SLDYNERLW--AWESWRESVGLQ 176  
 Db 183 SSHYDIIVASISIPPEQGVVLSAGAFNKGMDPKVRETLFAWE-----BAWKEK 238  
 Qy 177 RPLYEYVVLKNEMARAHYEDYDYGWRGVYGVNGVDYDYSRGQLIEDVEHTFEIKPL 236  
 Db 239 APLFTDTL-----NHLQGR---LSDYELHGVV--DFLQ-----KEL 270  
 Qy 237 YEHLHAYVRKLMNAYPSYISPIGCLPAHLGLDMWGRFTNLSLTVPFQKPNIDVTD 296  
 Db 271 -----EYNRLK-----KETLSVMWDTIQKNKQPLVNYLTRKANLFGKEK 309  
 Qy 297 MVDAQDAQRI-----PKAEKFPV-----SVGLPNNMTQGFWNSML---TDPG 337  
 Db 310 MEWQDQDAPIILLGLDKETFSFDEAAAFIENWKFSPMAKFAQSAPEKSWIEADRP 369  
 Qy 338 NVQKAVCHPTANDLGKGFPRILMCTKVTMDDFLTAHEMCHIYDYMAYAAQPFLLNGAN 397  
 Db 370 KRPGGYC--TELPETK--ESRIFMTYSKSNVEVATLAHELGHAFHSSTMDLPSL---N 421  
 Qy 398 EGFHBAVGEMISLSA-----ATPKHLSIGLLSPDFQEDNTEINFL---LQOALTI 448  
 Db 422 REYAMNVAETASTFAELIVADATLKVAKT-----KEEKINLDTKLQNALAMFM 470  
 Qy 449 TLPTTYMLE--KWRMVFKEIPKQMKWEMKREIVGVVPEVPHDEYCDPASLFHVS 507  
 Db 471 NIHSRIFENRYEARQGLVSEDKIEMMVYEAQKE--GYQGLATYHYFYFAAKLHFFI 528  
 Qy 508 NDYSFIRY-YTTLTYQFOFOEALQAAKHEG 537  
 Db 529 DNVFFYNFPYT---FGYLFSLGIYAYANQKG 556

Search completed: February 19, 2004, 19:52:14  
 Job time : 24 secs